

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:51:56 ; Search time 22.23 Seconds
(without alignments)
1475.375 Million cell updates

Title: US-09-236-468A-2
 Perfect score: 2907
 Sequence: 1 MAWLGCASLHVWCWGLMLGSCL.....DDILMEKPSRPMESNPDTTEG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	2907	100.0	541	18	AAW12695	G-protein parathyr	
2	2635	90.6	550	22	AAAB71875	Human PTH2 seven t	
3	2626	90.3	550	22	AAAB80560	Human PTH2 recepto	
4	2217.5	76.3	546	22	AAAB80559	Rat PTH2 receptor	
5	1418.5	48.8	536	21	AAAY96600	zebrafish parathyr	
6	1418.5	48.8	536	21	AAAY90230	zebrafish PTH1R re	
7	1392	47.9	585	17	AAAG2276	Opomuss kidney PTH	
8	1392	47.9	585	20	AAW73315	Parathyroid hormon	
9	1391	47.9	585	13	AAAR27705	Opomuss kidney PTH	
10	1388	47.7	515	17	AAAG92275	Opomuss kidney PTH	
11	1388	47.7	515	20	AAW73314	Parathyroid hormon	

12	1375	47.3	515	13	AA8277704	Opossum kidney PTH
13	1336.5	46.0	593	22	AA8718276	Human PTHR seven t
14	1331.5	45.8	591	17	AA8922277	Rat bone PTH/PTHrP
15	1331.5	45.8	591	20	AA8733116	Parathyroid hormon
16	1331.5	45.8	593	20	AAW73317	Human Parathyroid
17	1323.5	45.5	591	13	AA8277706	Rat bone PTH/PTHrP
18	1313	45.2	593	17	AA8922278	Human kidney PTH/P
19	1307.5	45.0	542	21	AAV956601	zebrafish parathy
20	1303.5	44.8	614	13	AA8277707	Human kidney PTH/P
21	1302.5	44.8	523	21	AAV902321	zebrafish PTH3R re
22	1043	35.9	448	21	AAV969886	Human tethered PTH
23	1043	35.9	450	21	AAV969888	Human tethered PTH
24	1041	35.8	435	21	AAV969887	Human tethered PTH
25	1038	35.7	446	21	AAV969893	Tethered PTH-1 rec
26	1036	35.6	435	21	AA807529	A mutant parathyro
27	1007.5	34.7	335	21	AAV969884	Tethered PTH-1 rec
28	1005.5	34.6	324	21	AAV969885	Tethered PTH-1 rec
29	801	27.6	449	13	AA830187	Secretin receptor:
30	785	27.0	458	16	AA8723506	Porcine vasoactive
31	784	27.0	440	22	AA871877	Human SCRC seven t
32	776	26.7	440	21	AA808188	Amino acid sequenc
33	772.5	26.6	459	14	AA842848	VIP receptor prote
34	759.5	26.1	457	22	AA871878	Human VIPR seven t
35	731	25.1	419	22	AA819881	Chicken growth hor
36	713.5	24.5	437	19	AA880309	Rat PACAP/VIP R-2
37	713.5	24.5	437	20	AA8922973	Rat PACAP/VIP R-2
38	708	24.4	437	16	AA870136	Rat vasoactive int
39	704	24.2	431	19	AAW80310	Human PACAP/VIP R-
40	704	24.2	431	20	AA8922974	Human PACAP/VIP R2
41	702.5	24.2	438	19	AA880308	Human PACAP/VIP R-
42	702.5	24.2	438	20	AA8922972	Human PACAP/VIP R-
43	702	24.1	438	22	AA871879	Human VIPs seven t
44	696.5	24.0	448	15	AA858666	Rat PACAP receptor
45	696.5	24.0	467	15	AA858656	Rat PACAP receptor

ALIGNMENTS

RESULT 1	
AAW12695	
ID	AAW12695 standard; Protein; 541 AA.
XX	
XX	
AC	AAW12695;
XX	
DT	31-MAY-1997 (first entry)
XX	
DE	G-protein parathyroid hormone receptor HLTG74.

G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
 calcium; signal transduction; agonist; antagonist; hypocalcaemia;
 hyperphosphataemia; hypoparathyroidism; chronic tetany;
 osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;
 kidney stone; nephrolithiasis; therapy; diagnosis.

XX OS	Homo sapiens.	
XX XX		
XX PN	WO9639433-A1.	
XX XX		
XX PD	12-DEC-1996.	
XX XX		
XX PF	05-JUN-1995;	95WO-US07085.
XX PR	05-JUN-1995;	95WO-US07085.
XX PA	(HUMA-) HUMAN GENOME SCI INC.	
XX XX		
XX PI	Li Y, Rosen CA, Ruben SM, Soppet DR;	
XX DR	WPI; 1997-043068/04.	
XX DR	N-PSDB; AAT59619.	
XX XX		
XX PT	Human G-protein parathroid hormone rec	

PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcaemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
PS Claim 9; Fig 1A-E; 62pp; English.

XX A novel 7-transmembrane receptor (AAW12695) has been identified as a
XX human G-protein parathyroid hormone (PTH) receptor, designated
CC HLTDG74. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AAW59619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTDG74 can be produced in transformed host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephrolithiasis.

XX Sequence 541 AA;

Query Match 100.0%; Score 2907; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLASLHWGMLGSCLLARAQLDSGDTITIEQIVLVKAKVQCELNITIAQLQEGE 60
DB 1 mawlgaslhvwmglsgscllaraqldsdgtitieqivlvkavqcelnitaqlqege 60
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTTWA 120
DB 61 gncfpewdglcwpgrgtgkisavpcppyiydfnhkgvafrcnpgntwdfmhslnkttwa 120
QY 121 NYSDCRLRFLOPDISICKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
DB 121 nysdcrlrflopdiskqecerlyvmytvgyisfsgslavailiigyfrlhlctrnyih 180
QY 181 MHLFVSFMLRATSFIVKDRVVAHIGVKELESIMODDPONSIEATSVDKSQYIGCKIAV 240
DB 181 mhlvsvfmlratsifvkdrrvvahigvkeleslimoddpnseatsvdksqyigckia 240
QY 241 VMTIYFLATNYWILVEGLYHNLIFVAFSDTKYILWGFTILGWGFPAAFAVAWAVARAT 300
DB 241 vmtiyflatnywvllvegylhnlifvafsdtkylwgftilgwgfpaafvaawavarat 300
QY 301 LADARCELSAGDIKWTYQAPILAAIGLNFILFLNTRVRLATKIWETNAVGHDTKQYRK 360
DB 301 ladarcelsagdikwtlyqapilaaiglnfiflntvrvlatkiwetnavghdtrkqyrk 360
QY 361 LAKSTLVLVLFVGVHIVFVCLPHSFSTGLWEIRHCELFNFNSFGFFVSIICYCNGEV 420
DB 361 lakstlvlvlfvgvhyivfvclphsftglweirhceelfnfsfgffvsiicycng 420
QY 421 QAEVKMWSRWNLSDWKRTPPCGSRRCGSVLTVTYHSTSSQVAAAHAWCLSLAKLPR 480
DB 421 qaevkmsrwnlsdwwkrtppcgsrrcgsvltvtvtyhstssqvaahawclslaklpr 480
QY 481 SPADSLTATSLYLAMSGVTSQTSRHTSLSPRSNKEDSGRQDDILMEKSPRMESNPDT 540
DB 481 spadsltatslylamsgvtsqtsrhtslsprsnkedsgrqddilmeksprmesnpdte 540
QY 541 G 541
DB 541 g 541

RESULT 2
AAB71875
ID AAB71875 standard; Protein; 550 AA.
XX
AC AAB71875;
XX
DT 03-MAY-2001 (first entry)

XX Human PTR2 seven transmembrane domain.

XX
KW Human; PTR2; parathyroid hormone receptor; h15571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
KW graft rejection; cystic fibrosis.

XX Homo sapiens.

XX WO200109328-A1.

XX 08-FEB-2001.

XX 03-AUG-2000; 2000WO-US21278.

XX 03-AUG-1999; 99US-0146916.

XX 29-FEB-2000; 2000US-0515781.

XX (MILL-) MILLENNIUM PHARM INC.

XX Hodge MR, Lloyd C, Weich NS;

XX WPI; 2001-138653/14.

XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX Disclosure; Fig 2; 145pp; English.

XX The present sequence is a human G-protein coupled receptor (GPCR) used
for comparison with the seven transmembrane domain of a novel GPCR
designated h15571. h15571 GPCR polynucleotides and polypeptides may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.

XX Sequence 550 AA;

Query Match 90.6%; Score 2635; DB 22; Length 550;
Best Local Similarity 91.4%; Pred. No. 2.3e-277;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

QY 1 MAWLGLASLHWGMLGSCLLARAQLDSGDTITIEQIVLVKAKVQCELNITIAQLQEGE 60
DB 1 mawlgaslhvwmglsgscllaraqldsdgtitieqivlvkavqcelnitaqlqege 60
QY 61 GNCFPEDWGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTTWA 120
DB 61 gncfpewdglcwpgrgtgkisavpcppyiydfnhkgvafrcnpgntwdfmhslnkttwa 120
QY 121 NYSDCRLRFLOPDISICKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYYIH 180
DB 121 nysdcrlrflopdiskqecerlyvmytvgyisfsgslavailiigyfrlhlctrnyih 180
QY 181 MHLFVSFMLRATSFIVKDRVVAHIGVKELESIMODDPONSIEATSVDKSQYIGCKIAV 240
DB 181 mhlvsvfmlratsifvkdrrvvahigvkeleslimoddpnseatsvdksqyigckia 240

Qy 241 VMFYFLATNYWIIWEGLYLHNLIFVAFESDTKYLMWGFILIGWGFPAAFVAANAVARAT 300
 Db 241 VMFYFLATNYWIIWEGLYLHNLIFVAFESDTKYLMWGFILIGWGFPAAFVAANAVARAT 300
 Qy 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360
 Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWELRHMCELFNSFGFVSIYCYCNGEV 420
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWELRHMCELFNSFGFVSIYCYCNGEV 420
 Qy 421 QAEVKKMSRWNLSDVDMKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477
 Db 421 QAEVKKMSRWNLSDVDMKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477
 Qy 478 LPRSPADSLTATSLYLSAMSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534
 Db 478 LPRSPADSLTATSLYLSAMSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534
 Qy 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmeKpsrpme 534
 Db 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmeKpsrpme 534
 Qy 535 SNPDTEG 541
 Db 535 SNPDTEG 541
 RESULT 3
 AAB80560
 ID AAB80560 standard; Protein; 550 AA.
 AC AAB80560;
 DT 26-APR-2001 (first entry)
 DE Human PTH2 receptor amino acid sequence.
 KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
 KW PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic;
 KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiac;
 KW cytosolic; antiasthmatic; neuroprotective; PTH receptor antagonist;
 KW obesity; eating disorder; metabolic disorder; mental disorder;
 KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
 KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
 KW hypertension; congestive heart failure; tumour; asthma; emphysema;
 KW restrictive lung disease; demyelinating condition; multiple sclerosis;
 KW leukodystrophy.
 OS Homo sapiens.
 XX WO200077042-A2.
 XX 21-DEC-2000.
 XX 15-JUN-2000; 2000WO-US16776.
 XX 15-JUN-1999; 99US-0139335.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Usdin TB, Hoare SRJ;
 XX WPI; 2001-122833/13.
 XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
 PT treating e.g. migraine or headaches, hypertension, obesity and other
 PT eating or metabolic disorders, mental disorders and osteoporosis -
 XX Example 4; Fig 1; 106pp; English.
 XX The present invention describes an isolated or purified peptide (I) that
 CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
 CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
 CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic, and

CC hypertensive, cardiant, cytostatic, antiasthmatic and neuroprotective
 CC activities, and is an PTH receptor antagonist. The peptide is useful in
 CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
 CC The PTH2 receptor binding activity may be used in treating obesity or
 CC other eating or metabolic disorders, mental disorders (e.g. depression,
 CC schizophrenia and dementia), acute or chronic pain, migraine or
 CC hypercalcaemia and other disorders affecting calcium metabolism,
 CC hypertension, congestive heart failure and control of tumour growth,
 CC asthma, emphysema or other restrictive lung diseases, and demyelinating
 CC conditions such as multiple sclerosis and leukodystrophies. The present
 CC sequence represents a PTH2 receptor which is used in the
 CC exemplification of the present invention.
 XX
 XX
 Qy Sequence 550 AA;
 Query Match 90.3%; Score 2626; DB 22; Length 550;
 Best Local Similarity 91.2%; Pred. No. 2.2e-276;
 Matches 499; Conservative 6; Mismatches 30; Indels 12; Gaps 3;
 Qy 1 MAWLGASLHVWGLMLGSCLLARALQDSGRTITIEQIVLVKAKVOCLELNTAOLGE 60
 Db 1 MAGIGASLHVWGLMLGSCLLARALQDSGRTITIEQIVLVKAKVOCLELNTAOLGE 60
 Qy 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRCNPNGTWDFMHSLNKTWA 120
 Db 61 GNCFFPNDGLICWPRGTGKISAVPCPPYIYDFNHNKGVAFRCNPNGTWDFMHSLNKTWA 120
 Qy 121 NYSCLRFQLPDDISIGKOEFCERLYVMTYVYSGISFGLAVAILIIGYFRRUHCRTNTH 180
 Db 121 NYSCLRFQLPDDISIGKOEFCERLYVMTYVYSGISFGLAVAILIIGYFRRUHCRTNTH 180
 Qy 181 MHLFVSFMLRATSIKQDFVVRVHAHIGVKELESIMQDDPQNSIEATSVDKSOYIGCKIAV 240
 Db 181 MHLFVSFMLRATSIKQDFVVRVHAHIGVKELESIMQDDPQNSIEATSVDKSOYIGCKIAV 240
 Qy 241 VMFYFLATNYWIIWEGLYLHNLIFVAFESDTKYLMWGFILIGWGFPAAFVAANAVARAT 300
 Db 241 VMFYFLATNYWIIWEGLYLHNLIFVAFESDTKYLMWGFILIGWGFPAAFVAANAVARAT 300
 Qy 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360
 Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRLATKIWETNAVGHDRKQYRK 360
 Qy 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWELRHMCELFNSFGFVSIYCYCNGEV 420
 Db 361 LAKSTLVLVVFGVHYIVFVCLPHSFTGLGWELRHMCELFNSFGFVSIYCYCNGEV 420
 Qy 421 QAEVKKMSRWNLSDVDMKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477
 Db 421 QAEVKKMSRWNLSDVDMKRTPCGSRRCGSLVTTVTHSTSSQSOVAAAHAMCL---SLAK 477
 Qy 478 LPRSPADSLTATSLYLSAMSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534
 Db 478 LPRSPADSLTATSLYLSAMSGVYQTSRTASHTLS---TRSNKEDSGRQRDDILMEKPSRPM 534
 Qy 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmeKpsrpme 534
 Db 481 IASRQPS-----hitlpgyvwnsnseqdciphsfheetkedsgrgddilmeKpsrpme 534
 Qy 535 SNPDTEG 541
 Db 535 SNPDTEG 541
 RESULT 4
 AAB80559
 ID AAB80559 standard; Protein; 546 AA.
 AC AAB80559;
 DT 26-APR-2001 (first entry)
 XX Rat PTH2 receptor amino acid sequence.
 DE Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
 KW

parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic; PTH2 receptor binding activity; antidepressant; neuroleptic; analgesic; antimigraine; antidiabetic; osteopathic; hypertensive; cardiac; cytotatic; antisthmatic; neuroprotective; PTH receptor antagonist; obesity; eating disorder; metabolic disorder; mental disorder; depression; schizophrenia; dementia; acute pain; chronic pain; migraine; headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism; hypertension; congestive heart failure; tumour; asthma; emphysema; restrictive lung disease; demyelinating condition; multiple sclerosis; leukodystrophy.

Rattus sp.

WO200077042-A2.

21-DEC-2000.

15-JUN-2000; 2000WO-US16776.

15-JUN-1999; 99US-0139335.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Usdin TB, Hoare SRJ;

WPI; 2001-122833/13.

New parathyroid hormone type 2 or 1 receptor ligand, useful for treating e.g. migraine or headaches, hypertension, obesity and other eating or metabolic disorders, mental disorders and osteoporosis -

Example 4; Fig I; 106pp; English.

The present invention describes an isolated or purified peptide (I) that is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1 receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant, nootropic, analgesic, antimigraine, antidiabetic, osteopathic, hypertensive, cardiac, cytotatic, antisthmatic and neuroprotective activities, and is an PTH receptor antagonist. The peptide is useful in the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor. The PTH2 receptor binding activity may be used in treating obesity or other eating or metabolic disorders, mental disorders (e.g. depression, schizophrenia and dementia), acute or chronic pain, migraine or headaches, diabetes and other metabolic disorders, osteoporosis, hypercalcaemia and other disorders affecting calcium metabolism, hypertension, congestive heart failure and control of tumour growth, asthma, emphysema or other restrictive lung diseases, and demyelinating conditions such as multiple sclerosis and leukodystrophies. The present sequence represents a PTH2 receptor which is used in the exemplification of the present invention.

Sequence 546 AA;

Query Match 76.3%; Score 2217.5; DB 22; Length 546;

Best Local Similarity 76.7%; Pred. No. 5.7e-232;

Matches 417; Conservative 37; Mismatches 81; Indels 9; Gaps 4;

QY 1 MAMLGASLHWGMLGSCLLARAQLDSDGTITIEQIVLVKAKVQCELNITAOQEGE 60

Db 1 mpwlealpycgwllrscilvgaqldsdgtlceeqivlmkkmqcelnitaqfge 60

QY 61 GNCFFPEOGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTWA 120

Db 61 gncfpwdglicwprtagtsampcpsyvdfnhkgvafhrctpgtwdflhgsnktwa 120

QY 121 NYSCLRFLOPDISGKQCEERLYVMYVGVISIFGSLAVAILLIIGYFRRLHCTRNTH 180

Db 121 nysdc--flqpdinlgkqeffenlylvtvgvisifgslavailliigyrfrlhctrnth 178

QY 181 MHLFVSFMLRATSIYFKDVRVHAHIGVKELESIMDDPQNSTEATSVDSKSYIGCKIAV 240

Db 179 ihlfvsmfmrmsifvkdvrvaqahlgvealslvmgdqlqnfiggpsvdkssqyvgckia 238

QY 241 VMFIYFLATNYWILVEGLYHLNLIFFVAFSDTKYLMGFIILGWGFPAAFAVAAMAVARAT 300
Db 239 vmfiyflatnywvillveglyhlhnlifsvfssdkylwgtllwgfpavfvvawavarat 298
QY 301 LADARCWELSGADIKWIQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRK 360
Db 299 ladtrcwelsagd-rwiyaqilaaiglnfilntvrvlatkietnavghdmrkyrk 357
QY 361 LAKSTLVLVLFVGVHVIVFVCLPHSFSTGLGWEIRMHCELFENSGFGFFVSIYCYCNGEV 420
Db 358 lakstlvvlvlfvgvhyivfvcqphsfsglweirmhcelffnsfgffvsiyycyngcv 417
QY 421 QAEVKMMSRWNLSDVMKRTPPCGSRRCGSLVLTTHSTSSQVAAAHAWCLSLAKLPR 480
Db 418 qaevkktwrnlswldwkkappcgghrygsvlttvtstssqgmppstrlvliasskpk 477
QY 481 SPA---DSLTAATSLYLAAMSGVTSQRTASHTLSRKNKESGRQRDILMEKFSRPMESNP 537
Db 478 tacrqldshvtlpgyvwssseqdcqps---tpeetckghgrqeddspvgessrpvafli 534
QY 538 DTEG 541
Db 535 dteg 538

RESULT 5

AAV99600

ID AAY99600 standard; Protein; 536 AA.

XX AAY99600;

AC AAY99600;

DT 27-OCT-2000 (first entry)

DE Zebrafish parathyroid hormone type-1 receptor PTH1R.

KW Zebrafish; parathyroid hormone type-1 receptor; PTH1R;

XX developmental disorder; physiological disorder; neurological disorder.

OS Brachydanio rerio.

PN WO200032775-A1.

PD 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28207.

PR 30-NOV-1998; 98US-0110467.

XX (JUEP/) JUEPPNER H.

PA (RUBI/) RUBIN D A.

XX Jueppner H, Rubin DA;

DR WPI; 2000-412323/35.

DR N-PSDB; AAA49625.

XX New nucleic acids encoding parathyroid hormone receptors PTH1R and PTH3R, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence -

PS Claim 17; Fig 2A; 11lpp; English.

XX The present sequence is the parathyroid hormone type-1 receptor

CC (PTH1R) from the zebrafish. Its coding sequence was obtained by

CC sequencing a cDNA clone. The gene and protein can be used to detect

CC diseases in man where the receptor is either overexpressed or

CC underexpressed, and they can be used to treat these diseases, which may

CC be developmental, physiological or neurological disorders. They can also

CC be used to identify agonists and antagonists which can be used in a

CC similar manner. In addition, the gene can be used for chromosome

CC identification.

[illegible]

Qy	342	TKIMETNAVGHDRKQYRKRLAKSTLVLVLVFGVHHYVVFCLPHS-FTGLGWETRMHCELP	400
Db	381	tklretnagrcdtrqykrllkstkltlvmplfgvhyivfmatpytevsgilwqvmhyeml	440
Qy	401	ENSFOGFVSVIILYCYCNCEVOAEVKKMSRWNLSDWKRTPPGSRRCGSLVLTIVTH---	457
Db	441	fnsqgfvaaliycfcngvevdaeiikkswrtlaidfkrkarsg-----stysygp	493
Qy	458	-STSGSOVAAAHAWCLSLAKLPRSPADSLTATSLYLAMSGVTQSRATSHTLSTRSKED	516
Db	494	vshstvnvgrgglalsls--prlapagasaanghqlpgvyknglsen-slpssgpe	550
Qy	517	SGRQRDDIIL-----EKPSRPMSNPDT	539
Db	551	pytkddgylngsglyepmvgeqppllleeret	583
RESULT	8		
AAW73315	ID	AAW73315 standard; Protein; 585 AA.	
XX	AC	AAW73315;	
XX	DT	08-FEB-1999 (first entry)	
XX	DE	Parathyroid hormone receptor OK-O.	
XX	KW	Parathyroid hormone receptor; PTH receptor; antibody; therapy;	
XX	KW	PTH-related hypercalcaemia; opossum.	
XX	OS	Didelphis virginiana.	
XX	PN	US5840853-A.	
XX	PD	24-NOV-1998.	
XX	FF	06-JUN-1995; 95US-0471494.	
XX	PR	06-APR-1992; 92US-0864475.	
XX	PR	05-APR-1991; 91US-0681702.	
XX	PR	06-JUN-1995; 95US-0471494.	
PA	(GENO)	GEN HOSPITAL CORP.	
PI	Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;		
PI	Schipani E, Segre GV;		
XX	WPI;	1999-034124/03.	
DR	N-PSDB;	AAV08389.	
XX	Antibody to parathyroid hormone receptor - for diagnostic or		
PT	therapeutic use		
XX	Claim 6; Fig 2; 63pp; English.		
XX	This sequence represents the opossum parathyroid hormone (PTH) receptor		
CC	OK-O, which is targeted by the antibody of the invention. The antibody		
CC	of the invention is immunoreactive with naturally occurring human, rat or		
CC	opossum PTH receptor. The antibody is useful for treating disorders		
CC	characterised by overstimulation of PTH receptors by their ligand and for		
CC	the diagnosis of PTH-related hypercalcaemia.		
XX			
SQ	Sequence	585 AA;	
Query Match	47.9%;	Score 1392;	DB 20; Length 585;
Best Local Similarity	47.8%;	Pred. No. 3.5e-14;	
Matches	274;	Conservative 92; Mismatches 137;	Indels 70; Gaps 9
Qy	24	AQLSDSGTITIEQIVLVKAKVQCELNITAOIQE	60
Db	24	alvdaddytkedilrrpaagcgegrkvelrvpelaesakdwmrsakttkkbaek	83

QY 61 -----GNCPEWDLICWPRCTGVKISAVPCPPYIYDFNHHKGVAFR 101
DB 84 lypqaeesrevsdrslqdgfcelpewdnivcwpagypkvavpcpdyfynhkggrayr 143
QY 102 HCNPNGTWDFMHSLNKNTWANYSDCLRFLOPDISIGKQFCERLYYMYTVGYISFGSLAV 161
DB 144 rcdsngswelvpnnrtwanysecvklfnetr--erevdfrlgmyltvgysislgstlv 201
QY 162 ATLIGYFRRLLHCTRNYTHMHLFVSMFLRATSFIVKDRVVAHIGVKELESIMQDDPON 221
DB 202 avllgyfrlthctnryihmhlfsfmlravsvfikkdavlsgvstdeleer-iteeela 260
QY 222 SIATSVDSKSOYIGCKIAVVMFIYPLATNYWILVEGLYHLNLFVAFPSDTKYLWGFIL 281
DB 261 fteppadkagfgrvartvlyflltnywlvegllyhslfmafsekylwgftl 320
QY 282 IGWGFPAFAVAAMAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLA 341
DB 321 fgwglpavfvavvtratlantecwdlssgnkklwlgvpillaaivvnfilfinirvla 380
QY 342 TKIWTNAVGHDTKQYRKLAKESTLVLVFGVHYIVFVCLPHS--FTGLGWEIRMHCELF 400
DB 381 tkiretngrcdtrqgrykllkstlvimpfvgvhyivfmatpctevsgllwqgmhyeml 440
QY 401 FNSFGFVSIYCYCNGEVOAEVKKMSRWNLSDWKRTPPCGSRRCGSLVTTVTH--- 457
DB 441 fnsfgffvailyfcngveqaeikksrwtlaidfkrkarsg-----stysyqpm 493
QY 458 -STSSQSOVAHAAMWCLSLAKLPRSPADSLTATSYLYAMSGVTQSRRTASHTLSTRNKED 516
DB 494 vshstvtvngprgglalsls--prlapgagasanghhlpgyvkhsisen-slpssgpe 550
QY 517 SGRQRDDILM-----EKPSRPMSNPDT 539
DB 551 pgtkddgylngsglyepmvgeqppplleeret 583

RESULT 9

AAR27705
ID AAR27705 standard; Protein; 585 AA.AC
XX

DT 16-MAR-1993 (first entry)

DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.

KW Parathyroid hormone; related protein; calcium; antagonist;

KW antibodies; hypercalcaemia.

OS Didelphis virginiana.

PN W09217602-A.

PD 15-OCT-1992.

PE 06-APR-1992; 92WO-US02821.

PR 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;

XX WPI; 1992-366271/44.

XX N-PSDB; AAQ29605.

XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours

XX PS Disclosure; Fig 2; 91pp; English.
XX CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
CC is identical to the OK-H clone except at the C-terminal tail as OK-O
CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
CC The difference is attributed to a single nucleotide deleted in the OK-H
CC sequence causing a frame shift and an earlier stop codon. It is not
CC known whether OK-O and OK-H represent prods. of two separate genes or
CC are a laboratory artifact. The protein may be used in a therapeutic
CC compsn. to inhibit activation of PTH or PTHrP and thus reduce the
CC level of calcium in the blood. Cpd. capable of competing with PTH
CC or PTHrP for binding can be identified using the protein prod. and
CC DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between a cell receptor and a
CC ligand such as in hypercalcaemia. See also AAR27704-16.
XX SQ Sequence 585 AA;

Query Match 47.9%; Score 1391; DB 13; Length 585;
Best Local Similarity 47.8%; Pred. No. 4.5e-142;
Matches 274; Conservative 93; Mismatches 136; Indels 70; Gaps 10;

QY 24 AQLSDGTITIEBQIVLVILKAKVQCELNIT----- 53
DB 24 alvdaddvltkeeqilllrnaqgeqlrkevtrvpelaesakdmsrsaktkekpaek 83
QY 54 --AQLQEG-----EGNCFPEWDLICWPRCTGVKISAVPCPPYIYDFNHHKGVAFR 101
DB 84 lypqaeesrevsdrslqdgfcelpewdnivcwpagypkvavpcpdyfynhkggrayr 143
QY 102 HCNPNGTWDFMHSLNKNTWANYSDCLRFLOPDISIGKQFCERLYYMYTVGYISFGSLAV 161
DB 144 rcdsngswelvpnnrtwanysecvklfnetr--erevdfrlgmyltvgysislgstlv 201
QY 162 ATLIGYFRRLLHCTRNYTHMHLFVSMFLRATSFIVKDRVVAHIGVKELESIMQDDPON 221
DB 202 avllgyfrlthctnryihmhlfsfmlravsvfikkdavlsgvstdeleer-iteeela 260
QY 222 SIATSVDSKSOYIGCKIAVVMFIYPLATNYWILVEGLYHLNLFVAFPSDTKYLWGFIL 281
DB 261 fteppadkagfgrvartvlyflltnywlvegllyhslfmafsekylwgftl 320
QY 282 IGWGFPAFAVAAMAVARATLADARCWELSGADIKWIYQAPILAAIGLNFILNTVRVLA 341
DB 321 fgwglpavfvavvtratlantecwdlssgnkklwlgvpillaaivvnfilfinirvla 380
QY 342 TKIWTNAVGHDTKQYRKLAKESTLVLVFGVHYIVFVCLPHS--FTGLGWEIRMHCELF 400
DB 381 tkiretngrcdtrqgrykllkstlvimpfvgvhyivfmatpctevsgllwqgmhyeml 440
QY 401 FNSFGFVSIYCYCNGEVOAEVKKMSRWNLSDWKRTPPCGSRRCGSLVTTVTH--- 457
DB 441 fnsfgffvailyfcngveqaeikksrwtlaidfkrkarsg-----stysyqpm 493
QY 458 -STSSQSOVAHAAMWCLSLAKLPRSPADSLTATSYLYAMSGVTQSRRTASHTLSTRNKED 516
DB 494 vshstvtvngprgglalsls--prlapgagasanghhlpgyvkhsisen-slpssgpe 550
QY 517 SGRQRDDILM-----EKPSRPMSNPDT 539
DB 551 pgtkddgylngsglyepmvgeqppplleeret 583

RESULT 10

AAR92275
ID AAR92275 standard; Protein; 515 AA.

XX

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AC AAR92275;
XX 18-MAY-1996 (first entry)
DE Opossum kidney PTH/PTHrP receptor.
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX Didelphis virginiana.
XX US5494806-A.
PN 27-FEB-1996.
XX 05-APR-1991; 91US-0681702.
XX 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
XX (GEO ) GEN HOSPITAL CORP.
XX PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX WPI; 1996-139028/14.
DR N-PSDB; AAT15945.
XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
XX Claim 1; Fig 1A-1E; 64pp; English.
PS Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
XX receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
CC separate genes or of a laboratory artifact. The receptor induces an
CC increase in intracellular cAMP and calcium when challenged with PTH or
CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
CC Host cells expressing the receptor can be used for diagnostic
CC measurement of PTH serum levels.
XX Sequence 515 AA;
SQ
Query Match 47.7%; Score 1388; DB 17; Length 515;
Best Local Similarity 54.6%; Pred. No. 7.9e-142;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
QY 24 AQLDSGTTTIEQIVLVLKAKVQCELTAAQLQEGE----- 60
Db 24 alvdaddvitkeeqiilllnaqaqcegrikevrlvpelaesaakdmsrsaktkekpaek 83
QY 61 -----GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFR 101
Db 84 lypqaesrevsdrslrldgfcfpewdnivcwpagvpgkvavpcpdyfydfnnhkgayr 143
QY 102 HCNPNCTWDFMHLNKTWANSYDCLRFLOPDISIGKQECERLYVMYTVGYSTISFGSLAV 161
Db 144 rcdsngswelpvgnrtwansysecvfltnetr--erevfdrlgmtyvtgyslsgsltv 201
QY 162 AILIGYFRRLHCTRNVIHMHLEFVSPLMRATSFVVKDRVHAHIGVKELESIMQDDPON 221
Db 202 avilgyfrlrhctryihmhlfvsmftravsfikdavlsvgsvtdeier-iteeelia 260
QY 222 SIATSVDKSOYIGCKTAVVMFTYELATNYWTLVSELVYLNLIYVAFSFDTKYLGWFTIL 281
Db 261 ftepppadkagrvgcavvtvlyfttnnywlvveglylhlslfmaffsekkylwgtl 320
QY 282 IGWGFPAEFAVAVARATLADARCWELSGAGDKWYIQAIPILAAIGLNFILFNTVVRVLA 341
Db 321 fggwlpavfvavvratlantecwldssgnkklqvpilaalvvnfilfinirvla 380
QY 342 TKIWTETNAVGHDTKQYRKAKSTLVLVVFGVHHVIVFVCLPHS-FTGLGWIRMHCELP 400
Db 381 tkiretnagrcdtrqgrkllkstvlmpifgvhyivfmatpytevgilwqvmhyeml 440
QY 401 FNSFGQFFVSIICYCNGEVQAEVKKMSRWNLSDVKRTPPCGS 445
Db 441 fnsfgqffvailyfcngevqaeikksrwlaldfkrkarsgs 485
RESULT 11
AAW73314
ID AAW73314 standard; Protein; 515 AA.
XX AC AAW73314;
XX 08-FEB-1999 (first entry)
XX Parathyroid hormone receptor OK-H.
XX Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; opossum.
XX Didelphis virginiana.
XX US5840853-A.
PN 24-NOV-1998.
XX 06-JUN-1995; 95US-0471494.
XX 06-APR-1992; 92US-0864475.
PR 05-APR-1991; 91US-0681702.
XX 06-JUN-1995; 95US-0471494.
XX (GEO ) GEN HOSPITAL CORP.
XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX WPI; 1999-034124/03.
DR N-PSDB; AAV08388.
XX Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
XX Claim 6; Fig 1; 63pp; English.
XX This sequence represents the opossum parathyroid hormone (PTH) receptor
CC OK-H, which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders
CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX Sequence 515 AA;
SQ
Query Match 47.7%; Score 1388; DB 20; Length 515;
Best Local Similarity 54.6%; Pred. No. 7.9e-142;
Matches 254; Conservative 73; Mismatches 92; Indels 46; Gaps 4;
QY 24 AQLDSGTTTIEQIVLVLKAKVQCELTAAQLQEGE----- 60
Db 24 alvdaddvitkeeqiilllnaqaqcegrikevrlvpelaesaakdmsrsaktkekpaek 83
QY 61 -----GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFR 101
Db 84 lypqaesrevsdrslrldgfcfpewdnivcwpagvpgkvavpcpdyfydfnnhkgayr 143

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Db	546	etlettppamaapkdgdflngscsglddeasgperpallqe	587
RESULT	14		
AAR92277			
ID	AAR92277	standard; Protein; 591 AA.	
XX	AC		
XX	AAR92277;		
XX	18-MAY-1996	(first entry)	
DT	DT		
XX			
DE	Rat bone PTH/PTHrP receptor.		
XX			
KW	Parathyroid hormone; receptor; parathormone; PTH;		
KW	Parathyroid hormone-related protein; PTHrP; calcium		
KW	hypercalcaemia; hypocalcaemia; cancer.		
XX			
OS	Rattus sp.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..192	
FT	Region	/label= Extracellular_region	
FT	Region	193..211	
FT	Region	/label= Transmembrane_region	
FT	Region	212..221	
FT	Region	/label= Intracellular_region	
FT	Region	222..240	
FT	Region	/label= Transmembrane_region	
FT	Region	241..299	
FT	Region	/label= Extracellular_region	
FT	Region	300..316	
FT	Region	/label= Transmembrane_region	
FT	Region	317..325	
FT	Region	/label= Intracellular_region	
FT	Region	326..342	
FT	Region	/label= Transmembrane_region	
FT	Region	343..364	
FT	Region	/label= Extracellular_region	
FT	Region	365..383	
FT	Region	/label= Transmembrane_region	
FT	Region	384..408	
FT	Region	/label= Intracellular_region	
FT	Region	409..428	
FT	Region	/label= Transmembrane_region	
FT	Region	429..444	
FT	Region	/label= Intracellular_region	
FT	Region	445..463	
FT	Region	/label= Transmembrane_region	
FT	Region	464..591	
FT	Region	/label= Intracellular_region	
XX			
PN	US5494806-A.		
XX			
PD	27-FEB-1996.		
XX			
PF	05-APR-1991;	91US-0681702.	
XX			
PR	06-APR-1992;	92US-0864475.	
PR	05-APR-1991;	91US-0681702.	
XX			
XX	(GEHO) GEN HOSPITAL CORP.		
PA			
XX	Abou-Samra A, Juppner H, Kronenberg HM, Potts JT		
PI	Schipani E, Segre GV;		
PI			
XX	WPI; 1996-139028/14.		
DR	N-PSDE; AAT15947.		
DR			
XX	DNA encoding vertebrate parathyroid hormone receptor		
PT	diagnosis and treatment of e.g. hypercalcaemia, hyp		
PT	cancer etc.		
XX			
PS	Claim 1; Fig 3A-3E; 64pp; English.		

Claim 1; Fig 3A-3E; 64pp; English.

XX A rat parathyroid hormone/parathyroid hormone-related protein
 CC (PTH/PTHrP) receptor (AAR92277) is encoded by cDNA clone R15B
 CC (AA15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library.
 CC The receptor is a G-protein linked receptor having 7 transmembrane
 CC domains. It induces an increase in intracellular cAMP and calcium
 CC upon challenge with PTH or PTHrP. Recombinant receptor can be
 CC produced in vector/host cell systems and used in the treatment,
 CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia,
 CC to screen for (ant)agonists and to raise antibodies. Host cells
 CC expressing the receptor are used for diagnostic measurement of PTH
 CC serum levels.
 XX
 SQ Sequence 591 AA;

Query Match 45.8%; Score 1331.5; DB 17; Length 591;
 Best Local Similarity 46.6%; Pred. No. 1.4e-135;
 Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;

Y 22 ARAQLSDGTITIEQIVLVKAKVOCE-----LNITAQLOEGEGN----- 62
 D 22 ayalvdaddvftkeeqifilhragaqcdkllkevlhtaanimdesdkwtpastsgkprke 81
 Y 63 -----CFPEWDGLICWPRGTGKISAVPCPPYIYDFNKH 96
 D 82 kasgkfypeskenkdvtgsrrrrgpcldpewdnivcplgaggevvavpcpdyiydfnkh 141
 Y 97 GVAFRHCNPGTWDFMHSLNKWTANYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISF 156
 D 142 ghayrrcdngswewvpgghrtwanyseclkmtnetr--erevfdrlgmlytvgymsl 199
 Y 157 GSLAVAILIIGFRRUHCRTNRYHMHILFVSFMLRATSIKVKDRVVAHVGKLESL--- 213
 D 200 asltvavilaylfrlhrctnrnyihmhflsmlraasifvkdavlysgftldeaeerltee 259
 Y 214 ----IMQDDPQNSIEATSDKSOYIGCKTAVVMFYFLATNYWILVEGLYLHNLIFVAF 269
 D 260 elhilaqvpvpppaaavg-----yagcrvavtfflylatnywvllvegllyhslifmaf 314
 Y 270 FSDTKYLWGFIITGWFPAAPFAAANAARATLADARCWELSGADIKWIYQAPILAAIGLN 329
 D 315 fsekylwgtifgwglpavvavvgratiantgcwldssghkwwilqvpilasvln 374
 Y 330 FILELNTVRLATKIWETNAVGHDRKQYKLAQSLVTLVLFVGVHYIVFVCLPHS-FTG 388
 D 375 filfinilrvtatkiretnagrcdtrqyrkllrstclvlplfgvhytvmalpytevsg 434
 Y 389 LGWEIRHMCLEFPNSFQGFVSIYCYCNGEVOAEVKMWRNLSVDWKRTTPPCGSRRC 448
 D 435 tlwqgmhyemlfnsgffvallycfngvgeqaeirksrwtaldfkrkarsgssy 494
 Y 449 GSVLTVTHSTSSQSOVAAAHAACLSLAKLPRSPADSLTATSLYLAMSG-----VTQS 501
 D 495 -sygpmvshstvtngprag----lslpsrlpp---attnghsqldpghakpgapatet 546
 Y 502 RTASHTLSTRS-----NKEDSGRQRDDILMEK 528
 D 547 eltpvtmavpkddgflngscsgldaeasgarpplliqe 585

RESULT 15
 ID AA073316
 ID AA073316 standard; Protein; 591 AA.
 XX
 AC AA073316;
 XX
 DT 08-FEB-1999 (first entry)
 XX
 DE Parathyroid hormone receptor R15B.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; rat.

XX Rattus sp.
 OS US5840853-A.
 PN 24-NOV-1998.
 PD 06-JUN-1995; 95US-0471494.
 PF 06-APR-1992; 92US-0864475.
 PR 05-APR-1991; 91US-0681702.
 PR 06-JUN-1995; 95US-0471494.
 XX (GEO) GEN HOSPITAL CORP.
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 DR N-PSDB; AAV08390.
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 PS Claim 6; Fig 3; 63pp; English.
 XX This sequence represents the rat parathyroid hormone (PTH) receptor
 CC R15B, which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX
 SQ Sequence 591 AA;

Query Match 45.8%; Score 1331.5; DB 20; Length 591;
 Best Local Similarity 46.6%; Pred. No. 1.4e-135;
 Matches 270; Conservative 86; Mismatches 136; Indels 87; Gaps 11;

Y 22 ARAQLSDGTITIEQIVLVKAKVOCE-----LNITAQLOEGEGN----- 62
 D 22 ayalvdaddvftkeeqifilhragaqcdkllkevlhtaanimdesdkwtpastsgkprke 81
 Y 63 -----CFPEWDGLICWPRGTGKISAVPCPPYIYDFNKH 96
 D 82 kasgkfypeskenkdvtgsrrrrgpcldpewdnivcplgaggevvavpcpdyiydfnkh 141
 Y 97 GVAFRHCNPGTWDFMHSLNKWTANYSDCLRFLOPDISIGKQFCERLYVMYTVGYSISF 156
 D 142 ghayrrcdngswewvpgghrtwanyseclkmtnetr--erevfdrlgmlytvgymsl 199
 Y 157 GSLAVAILIIGFRRUHCRTNRYHMHILFVSFMLRATSIKVKDRVVAHVGKLESL--- 213
 D 200 asltvavilaylfrlhrctnrnyihmhflsmlraasifvkdavlysgftldeaeerltee 259
 Y 214 ----IMQDDPQNSIEATSDKSOYIGCKTAVVMFYFLATNYWILVEGLYLHNLIFVAF 269
 D 260 elhilaqvpvpppaaavg-----yagcrvavtfflylatnywvllvegllyhslifmaf 314
 Y 270 FSDTKYLWGFIITGWFPAAPFAAANAARATLADARCWELSGADIKWIYQAPILAAIGLN 329
 D 315 fsekylwgtifgwglpavvavvgratiantgcwldssghkwwilqvpilasvln 374
 Y 330 FILELNTVRLATKIWETNAVGHDRKQYKLAQSLVTLVLFVGVHYIVFVCLPHS-FTG 388
 D 375 filfinilrvtatkiretnagrcdtrqyrkllrstclvlplfgvhytvmalpytevsg 434
 Y 389 LGWEIRHMCLEFPNSFQGFVSIYCYCNGEVOAEVKMWRNLSVDWKRTTPPCGSRRC 448
 D 435 tlwqgmhyemlfnsgffvallycfngvgeqaeirksrwtaldfkrkarsgssy 494
 Y 449 GSVLTVTHSTSSQSOVAAAHAACLSLAKLPRSPADSLTATSLYLAMSG-----VTQS 501

Db 495 -sygmvshstvtngvrag----lsiplsprlpp---atnghsqipghakpgapatet 546
Qy 502 RTASHTLSTRS-----NKEDSGRQDDILMEK 528
Db 547 etlpvtnavpkddgflngscsgldeasgsarpppliqe 585

Search completed: September 21, 2001, 17:05:44
Job time: 828 sec

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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:53:22 ; Search time 19.54 Seconds
(without alignments)
2109.029 Million cell updates/sec

Title: US-09-236-468a-2
Perfect score: 2907
Sequence: 1 MAWLGLASLHVWGLMLGSL.....DDILMEKPSRPMESNPDTG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2635	90.6	550	2 A57519	parathyroid hormon
2	1392	47.9	585	2 A39286	parathyroid hormon
3	1336.5	46.0	593	2 A49191	parathyroid hormon
4	1331.5	45.8	591	2 I34195	parathyroid hormon
5	1324	45.5	591	2 S44203	parathyroid hormon
6	1298.5	44.7	589	2 I59297	parathyroid hormon
7	801	27.6	449	2 S16319	secretin receptor
8	776	26.7	440	2 JC2532	secretin receptor
9	772.5	26.6	459	2 JH0594	vasoactive intesti
10	756	26.0	460	2 JC2194	vasoactive intesti
11	755.5	26.0	495	2 JC2195	vasoactive intesti
12	713.5	24.5	437	2 JU0185	PACAP/VIP receptor
13	708	24.4	437	2 S39069	vasoactive intesti
14	702	24.1	438	2 G02822	vasoactive intesti
15	696.5	24.0	467	2 JN0616	pituitary adenylat
16	689.5	23.7	525	2 JN0902	pituitary adenylat
17	682.5	23.5	495	2 S39061	pituitary adenylat
18	681.5	23.4	495	2 S36114	pituitary adenylat
19	673.5	23.2	513	2 S47631	pituitary adenylat
20	667.5	23.0	523	2 S39060	pituitary adenylat
21	662	22.8	462	2 JC2462	gastric inhibitory
22	655	22.5	463	2 A46172	glucagon-like pept
23	641.5	22.1	466	2 G02234	gastric inhibitory
24	641.5	22.1	466	2 S66676	glucose-dependent
25	630.5	21.7	463	2 I84494	glucagon-like pept
26	628.5	21.6	423	2 A45363	somatoliberin rece
27	620.5	21.3	463	2 S71624	glucagon-like pept
28	619	21.3	477	2 JC2041	glucagon receptor
29	618.5	21.3	381	2 S33449	pituitary adenylat

30	616	21.2	455	2 I53273	gastric inhibitory
31	612	21.1	451	2 I46586	growth hormone-rel
32	607	20.9	485	2 JQ1957	glucagon receptor
33	604	20.8	491	2 I37411	glucose-dependent
34	596.5	20.5	423	2 S29753	growth hormone-rel
35	595.5	20.5	474	2 I37217	calcitonin recepto
36	595	20.5	485	2 JC4363	glucagon receptor
37	589.5	20.3	515	2 I49154	calcitonin recepto
38	583.5	20.1	479	2 S33746	calcitonin recepto
39	579.5	19.9	490	2 S34486	calcitonin recepto
40	579	19.9	478	2 A37430	calcitonin recepto
41	576.5	19.8	515	2 I60800	calcitonin recepto
42	575	19.8	464	2 S29754	growth hormone-rel
43	557.5	19.2	482	2 A39285	calcitonin recepto
44	544.5	18.7	498	2 I47130	calcitonin recepto
45	541	18.6	431	2 I49149	CRF receptor - mou

ALIGNMENTS

RESULT 1

A57519
parathyroid hormone receptor 2 precursor - human
N:Alternate names: PTH2 receptor
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C:Accession: A57519
R:Usdin, T.B.; Gruber, C.; Bonner, T.I.
J. Biol. Chem. 270, 15455-15458, 1995
A:Title: Identification and functional expression of a receptor selectively recognizi
A:Reference number: A57519; MUID:95318121
A:Accession: A57519
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-350 <OSD>
A:Cross-references: GB:U25128; MID:9887966; PIDN:AAC50157.1; PID:9887967.
C:Genetics:
A:Gene: GDB:PTH2R2; PTHR2R
A:Cross-references: GDB:731977; OMIM:601469
A:Map position: 2q33-2q33
C:Superfamily: glucagon receptor
C:Keywords: hormone receptor

Query Match 90.6%; Score 2635; DB 2; Length 550;
Best Local Similarity 91.4%; Pred. No. 8.6e-214;
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;

Qy	1	MAWLGLASLHVWGLMLGSL	RAQLDSDGTTIEBQIVLVKAKVQCELNIT	QAQLEGE	60
Db	1	MAGLGLASLHVWGLMLGSL	RAQLDSDGTTIEBQIVLVKAKVQCELNIT	QAQLEGE	60
Qy	61	GNCFFPEWDGLICWPRGTGKISAVPCPPY	YDFNKHGVAFRHCPNPNGTWDFHSLNKTWA	120	
Db	61	GNCFFPEWDGLICWPRGTGKISAVPCPPY	YDFNKHGVAFRHCPNPNGTWDFHSLNKTWA	120	
Qy	121	NYSDCLRFLOPDISICKQFCERLYVMYTVG	YSISFGSLAVAILLIIGYFRLHCTNRYIH	180	
Db	121	NYSDCLRFLOPDISICKQFCERLYVMYTVG	YSISFGSLAVAILLIIGYFRLHCTNRYIH	180	
Qy	181	MHLFVSFMLRATSI	IFVKDRVVAHIGVKELESIMODDPQNSTEAT	SVDSQYIGCKIAV	240
Db	181	MHLFVSFMLRATSI	IFVKDRVVAHIGVKELESIMODDPQNSTEAT	SVDSQYIGCKIAV	240
Qy	241	VMFIYFLATNYWILVEGLYLHNLI	IFVAFSDTKYLMGFILIGWGFPAFAVAWAVARAT	300	
Db	241	VMFIYFLATNYWILVEGLYLHNLI	IFVAFSDTKYLMGFILIGWGFPAFAVAWAVARAT	300	
Qy	301	LADARCWELSGADIKWIYQAPILAAIGL	FNILFNTVRVLATKIWETNAVGHDTKQYRK	360	
Db	301	LADARCWELSGADIKWIYQAPILAAIGL	FNILFNTVRVLATKIWETNAVGHDTKQYRK	360	

RESULT 10
JC21194
vasoactive intestinal peptide receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C:Accession: JC21194; JN0604; PC2289; S38397
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-D
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDN
A:Reference number: JC21194; MUID:94235025
A:Accession: JC21194
A:Molecule type: mRNA
A:Residues: 1-460 <COU>
A:Cross-references: EMBL:X75299; NID:q407461; PIDN:CAA53046.1; PID:q407462
A:Experimental source: jejunal epithelial cell; clone hivr8
R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A:Title: Cloning and functional expression of a human neuroendocrine vasoactive inte
A:Reference number: JN0604; MUID:93290641
A:Accession: JN0604
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-284, 288-460 <SRE>
A:Cross-references: GB:L13288; NID:g292903; PIDN:AAA36805.1; PID:g292904
R:Couvineau, A.; Gaudin, J.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe,

Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A:Reference number: PC2289; MUID:95118345
A:Accession: PC2289
A:Molecule type: mRNA
A:Residues: 63-129 <CO>
C:Genetics:
A:Gene: GDB:VIPR1; RCD1; HVRI
A:Cross-references: GDB:128589; OMIM:192321
A:Map position: 3p22-3p22
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F:145-168/Domain: transmembrane #status predicted <TM1>
F:176-194/Domain: transmembrane #status predicted <TM2>
F:216-234/Domain: transmembrane #status predicted <TM3>
F:255-277/Domain: transmembrane #status predicted <TM4>
F:299-319/Domain: transmembrane #status predicted <TM5>
F:346-363/Domain: transmembrane #status predicted <TM6>
F:377-396/Domain: transmembrane #status predicted <TM7>
F:58.69.100.293/Binding site: carboxylate (Asn) (covalent) #status predicted
F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 26.0%; Score 756; DB 2; Length 460;
Best Local Similarity 36.1%; Pred No. 8e-56;
Matches 180; Conservative 80; Mismatches 144; Indels 94; Gaps 20;

QY 13 WMLGSLARQLDSG-----TITIEQIVLVKAKVOCELENI-TAQLOEGEGNCFPE 66
Db 11 WL-----CVLAGALAWALGPAGQAARLQECDDYQVQIEVQKQLEAEQLENETIGCSKM 66
QY 67 WDLGLCPRGTVGKISAVPCPPYIDFNH---KGVAFRHCNPNGTWDFMHSLNKWTWANS 123
Db 67 WDLNLCTWPATPRGQVVLACPLFKLFSSIQGRNV-SRCTDEG-----WTH-- 112
QY 124 DCLRFQPD-----ISIGKQE--FCERLYVMYTVGYSIFSGSLAVAILIIGYF 169
Db 113 -----LEPGPYTACGLDDKAASLDQQTWFYGSVKTYGTYGLSLATLLVATILSLF 167
QY 170 RLHCTRNTHHMLFVSMRLATSIPIVKDRVHAHIGVKELESIMQDDPQNSIEATSD 229
Db 168 RKLHCTRNTHHMLFTSILRAAAVFIKDLALF-----DSGESDQCS 209
QY 230 KSOYIGCKTAVVMFYFLATNYWILVEGLYLNHLIFVAFESDTKYLWGIFILGWGFPAA 289
Db 210 EGS-VGCKAAMVFFQYCVMANFWLLVEGLYLYTLAVSFSEKRYFWGILGWGVPST 268
QY 290 FYAAMAVARATLAD---ARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLATKIWE 346
Db 269 FTWVWTIARHEDYGLLRCWDTINSSLMWIKGPILTSLVNFILFICIRILLQKLRP 328
QY 347 TNAVGHDTTRKQ----YRKLAESTLVLVVFGVHYIVFVCLPHSFTGLGWIRHMCLEFPN 402
Db 329 P-----DIRKSDSSPSRLARSTLLIPLFGVHYIMFAFFPDNFKP---EVKMFVFLVVG 380
QY 403 SFQGFVSIYCYCNCEVAEKKMSRNLS--VDWK---RTPPCGSR--RCG----SVL 452
Db 381 SFQGFVVALYLCFLNGEVAELRRKRRHQLGVGLGNPKYRHPSGSGSGNGATCSTQVSM 440
QY 453 TTVT----HSTSSOSOVA 466
Db 441 TRVSPGARRSSSQAEVS 458

RESULT 11
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone hivr5) - human
C:Species: homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999

C:Accession: JC2195; S42087
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-De
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA
A:Reference number: JC2194; MUID:94235025
A:Accession: JC2195
A:Molecule type: mRNA
A:Residues: 1-495 <COU>
A:Cross-references: EMBL:X77777; NID:q456352; PIDN:CAA54814.1; PID:q456353
A:Experimental source: jejunal epithelial cell
C:Genetics:
A:Gene: GDB:VIPR1; RCD1; HVRI
A:Cross-references: GDB:128589; OMIM:192321
A:Map position: 3p22-3p22
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-495/Product: vasoactive intestinal peptide receptor-related protein #status pred
F:180-203/Domain: transmembrane #status predicted <TM1>
F:211-229/Domain: transmembrane #status predicted <TM2>
F:251-269/Domain: transmembrane #status predicted <TM3>
F:290-312/Domain: transmembrane #status predicted <TM4>
F:334-354/Domain: transmembrane #status predicted <TM5>
F:381-398/Domain: transmembrane #status predicted <TM6>
F:412-431/Domain: transmembrane #status predicted <TM7>
F:93.104.135.328/Binding site: carboxylate (Asn) (covalent) #status predicted
F:111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F:285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 26.0%; Score 755.5; DB 2; Length 495;
Best Local Similarity 36.6%; Pred. No. 9.6e-56;
Matches 177; Conservative 80; Mismatches 138; Indels 89; Gaps 19;

QY 22 ARAQLDSGCTIIEQIVLVKAKVOCELENI-TAQLOEGEGNCFPEWDLGICWPRGTGK 80
Db 60 ARSLGSG---SLQECDDYQVQIEVQKQLEAEQLENETIGCSKMDNLCTWCPATPRGQ 115
QY 81 ISAVPCPPYIDFNH---KGVAFRHCNPNGTWDFMHSLNKWTWANSYDCLRFQPD---- 132
Db 116 VVVLACPLFKLFSSIQGRNV-SRCTDEG-----WTH-----LEPGPYPIA 156
QY 133 -----ISIGKQE--FCERLYVMYTVGYSIFSGSLAVAILIIGYPRRLHCTRNTHHML 183
Db 157 CGLDDKAASLDQQTWFYGSVKTYGTYGTYGLSLATLLVATILSLFRKLHCTRNTHHML 216
QY 184 FVSFMLRATSIPIVKDRVHAHIGVKELESIMQDDPQNSIEATSDVKSOYIGCKIAVWVF 243
Db 217 FISFILRAAAVFIKDLALF-----DSGESDQCSGSG-VGCKAAMVFF 257
QY 244 IYFLATNYWILVEGLYLNHLIFVAFESDTKYLWGIFILGWGFPAAVAAVARATLAD 303
Db 258 QYCVMANFWLLVEGLYLYTLAVSFSEKRYFWGILGWGVPSTFTWVWTIARHED 317
QY 304 ---ARCWELSGADIKWYQAPILAAIGLNFILFNTVRVLATKIWEAVGHDTTRKQ--- 357
Db 318 YGLLRCDWTINSSLMWIKGPILTSLVNFILFICIRILLQKLRP-----DIRKSDSS 372
QY 358 -YRKLAESTLVLVVFGVHYIVFVCLPHSFTGLGWIRHMCLEFPNSFGFFVSIYCYC 416
Db 373 PYSRLARSTLLIPLFGVHYIMFAFFPDNFKP---EVKMFVFLVVGSGFGVVALYCYFL 429
QY 417 NGEVQAEVKKMSRNLS--VDWK---RTPPCGSR--RCG---SVLTVT---HSTSSQ 462
Db 430 NGEVQAEELRRKRRHQLGVGLGNPKYRHPSGSGSGNGATCSTQVSMLTRVSPGARRSSSQ 489
QY 463 SQVA 466
Db 490 AEVS 493

RESULT 12

JU0185

PACAP/VIP receptor (PACAPR-3) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C:Accession: A53471; JU0185
R:Inagaki, N.; Yoshida, H.; Mizuta, M.; Mizuno, N.; Fujii, Y.; Gonoi, T.; Miyazaki, J.;
Proc. Natl. Acad. Sci. U.S.A. 91, 2679-2683, 1994
A:Title: Cloning and functional characterization of a third pituitary adenylate cyclase-
A:Reference number: A53471; MUID:94195806
A:Accession: A53471
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-437 <RES>
A:Cross-references: GB:D28132; NID:9473721; PIDN:BAA05674.1; PID:g496376
A:Experimental source: strain C57BL/6
C:Superfamily: glucagon receptor
C:Keywords: receptor

Query Match 24.5%; Score 713.5; DB 2; Length 437;
Best Local Similarity 33.6%; Pred. No. 2.8e-52;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;

QY 39 VLVLKAKVQCELNITAOLOEGEGNCFP-----EWGLICWPRGTVCKISAV 84

Db 13 LLVRSSIHPCRFHLEIQEEETKCAELLSSQTNORACSGWQDNITCWRPADVGETTV 72

QY 85 PCPPVIYDF-NHKGVAFRHCNPGTWDPMHSLNKTWANSCLRFLOPDISIGKQEFCE 143

Db 73 PCPKVFSNFSRPGNISKNCTSDG-W-----SETFPDFIDACGYNDPE-DESKISFYL 124

QY 144 LVYMTVGYSGISFGSLAVAILIIGYFRRLHCTRNYYIHMHLFVSPMLRATSIFFVDRVVHA 203

Db 125 VKAIYTLGYSVLSLSTGSIICLFKRLHCTRNYYIHMHLFVSPMLRATSIFFVDRVVHA 184

QY 204 HIGVKELESIMQDDPQNSIATSVDRKSOYIGCKIAVVMFYFLATNYWILVEGLYLNH 263

Db 185 SSSL-----LRCHDOP-----ASWVGCKLSLVFFQYCIWANEFYLLVEGLYLHT 228

QY 264 LIEVAFFSDTYLWGLFILLIGWGEFAAFAVARATLADARCWELSGADIK-WIYQAPI 322

Db 229 LL-VAILPPSRCLFLAYLLIGWGEFVSGICGATWATRLSLEDTCGWDNDHSIPWVIRMPI 287

QY 323 LAALGLNFIPLNTVRVLTATKIWETNAVGHTRKQYKRLAKSTLVLVFVGHVYIVFYCL 382

Db 288 LISIWNFALFISIVRILLQKLTSPDVGND-QSQYKRLAKSTLLIPLFCGVHVMVPAAF 346

QY 383 PHSTGTGLWEIRMHCELFNFSQGFYFIIYCYNGEVOAEVKMWSRWNLSDVKRTPP 442

Db 347 P---IGISSTYQIILFELCVGSGFQGLVAVLYCFLNSEVQCELRKRW----- 390

QY 443 CGSRRCGSLVTVTHTSSQSOVAHAACLSLAKLPRSPADSLTATSLYLAMSGVTQSR 502

Db 391 -----GLCL-----TQAGSRDYLHWSMS-----RNGSES-----ALQIHRSRTQSF 429

QY 503 TASHT 507

Db 430 LQSET 434

RESULT 13

S39069

vasoactive intestinal peptide receptor vip2 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999

C:Accession: S39069

R:Lutz, E.M.; Sheward, W.J.; West, K.M.; Morrow, J.A.; Fink, G.; Harmar, A.J.

FEBS Lett. 334, 3-8, 1993

A:Title: The VIP(2) receptor: molecular characterisation of a cDNA encoding a novel rec

A:Reference number: S39069; MUID:94039806

A:Accession: S39069

A:Molecule type: mRNA

A:Residues: 1-437 <LUT>

A:Cross-references: EMBL:Z25885; NID:g414188; PIDN:CAA81104.1; PID:g414189
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; intestine; transmembrane protein

Query Match 24.4%; Score 708; DB 2; Length 437;
Best Local Similarity 33.9%; Pred. No. 8.2e-52;

Matches 159; Conservative 89; Mismatches 155; Indels 66; Gaps 15;

QY 41 VLKAKVQCELNITAOLOEGEGNCFPEWGLICWPRGTVGKISAVPCPPVIYDF-NHKGVA 99

Db 30 IQEETKCAELLSSQ-NHRCACSGWQDNITCWRPADIGETVPCPVFSNFSRPGNI 88

QY 100 FRHCNPGTWDPMHSLNKTWANSCLRFLOPDISIGKQEFCEERLYVMYTVGYSGISFGSL 159

Db 89 SKNCTSDG-W-----SETFPDFIDACGYNDPE-DESKITFYLVKAIYTLGYSVLSLMSL 140

QY 160 AVAILIIGYFRRLHCTRNYYIHMHLFVSPMLRATSIFFVDRVVHAHIGVKELESIMQDDP 219

Db 141 TTGSIICLFKRLHCTRNYYIHMHLFVSPMLRAISLVLRKDSVLYSSG-----TLRCHDOP 195

QY 220 QNSTEATSVDRKSOYIGCKIAVVMFYFLATNYWILVEGLYLNHLEIFVAFTSDTYLWGLF 279

Db 196 -----GSWVGCKLSLVFFQYCIWANEFYLLVEGLYLHTLL-VAILPPSRCLFLAY 243

QY 280 ILIGWGEFAAFAVARATLADARCWELSGADIK-WIYQAPILAALGLNFIPLNTVR 338

Db 244 LLIGWGEFVSGICGATWATRLSLEDTCGWDNDHSIPWVIRMPIILISIVNFAFISIVR 303

QY 339 VLTATKIWETNAVGHTRKQYKRLAKSTLVLVFVGHVYIVFYCLPHSTGTGLWEIRMHCE 398

Db 304 ILLQKLTSPDVGND-QSQYKRLAKSTLLIPLFCGVHVMVPAAF---IGISSTYQIILFE 359

QY 399 LFFNSQGFYFIIYCYNGEVOAEVKMWSRWNLSDVKRTPPCGSRRCGSLVTVTHTS 458

Db 360 LCVGSGFQGLVAVLYCFLNSEVQCELRKRW-----GLCL----- 394

QY 459 TSSQSOVAHAACLSLAKLPRSPADSLTATSLYLAMSGVTQSR TASHT 507

Db 395 TOPGSRDYLHWSMS-----RNGSES-----ALQIHRSRTQSF LQSET 434

RESULT 14

G02822

vasoactive intestinal peptide receptor 2 - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Jun-2000

C:Accession: G02822; JC2463

R:Lutz, E.M.

submitted to the EMBL Data Library, January 1996

A:Reference number: H01736

A:Accession: G02822

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-438 <LUT>

A:Cross-references: EMBL:X95097; NID:g1160469; PIDN:CAA64474.1; PID:g1160470

R:Syoboda, M.; Tastenoy, M.; Van Rampelbergh, J.; Goossens, J.F.; De Neef, P.; Waelbr

Biochem. Biophys. Res. Commun. 205, 1617-1624, 1994

A:Title: Molecular cloning and functional characterization of a human VIP receptor fr

A:Reference number: JC2463; MUID:95110300

A:Accession: JC2463

A:Molecule type: mRNA

A:Residues: 1-38, 'T', 40-411, 'H', 413-423, 'A', 425-438 <SVO>

A:Cross-references: GB:L36566; NID:g550477; PIDN:AAC37569.1; PID:g550478

A:Experimental source: SUP-T1 lymphoblast cell line

C:Genetics:

A:Gene: GDB:VIPR2

A:Cross-references: GDB:335025

A:Map position: 7q36.3-7q36.3

C:Superfamily: glucagon receptor

C:Keywords: glycoprotein; intestine; receptor; transmembrane protein

F:130-150/Domain: transmembrane #status predicted <TM1>

F:160-179/Domain: transmembrane #status predicted <TM2>

F;206-228/Domain: transmembrane #status predicted <TM3>
F;241-262/Domain: transmembrane #status predicted <TM4>
F;282-304/Domain: transmembrane #status predicted <TM5>
F;329-349/Domain: transmembrane #status predicted <TM6>
F;361-384/Domain: transmembrane #status predicted <TM7>
F;59,88,92/Binding site: carbohydrate (Asn) #status predicted

Query Match 24.1%; Score 702; DB 2; Length 438;
Best Local Similarity 36.1%; Pred. No. 2.6e-51;
Matches 150; Conservative 84; Mismatches 138; Indels 44; Gaps 14;

QY 41 VLKAKVOCENITQAQLOGEGNCFEPWDLGGLICRGTGVTKGISAVPCPPYYIDFNHK-GVA 99
:
Db 31 IOEBETKCAELLSQTKEHKA-CSGVWDNTTCRPANVGTTVPCKVFNSFYSKAGNI 89
:
QY 100 FRHCNPNGTWFMSHLNKTWANYSDCLRFLOPDISICKQECERLYVMYTVGYSGISFGSL 159
:
Db 90 SKNCTSDG-W-----SETPDFDADCGYSDE--DESKIIFYILVKAIYLIGSVSLSML 141
:
QY 160 AVAILIYGFRRLCHTRNYIHMHLEFVSFMLRASTIFKYDRVVHAHIGVKELESIMODDP 219
:
Db 142 ATGSIIILCFLRKLCRTNRNYIHLNLFLSFILRAISVLVKDDVLYSSG-----TLRGPDQP 196
:
QY 220 QNSTEATSVDKSQYIGCKIAVMMFIYFLATNYWILVEGLYLNLIIFVAFSDFTKYLWGF 279
:
Db 197 -----SSWGCKLSLVFYQYCIAMNFLLVEGLYLHTLL-VAMLPPRRCEFLAY 244
:
QY 280 ILIGWFPAAFAAWAVARATLADARCWELSAGDIK-WIQOAPILAALGNLFILFLNTVR 338
:
Db 245 LLIGWGLPTVCIGAWTAARLYLEDTGCWDNDHSVPMWRIRIPILISIIVNFVLFISIR 304
:
QY 339 VLAPTKIWNETHNAVDHTRKQYRKLAKSTLVLLVLFVGVHYIVFCVLPSPHSTGLGWSEIRMHCE 398
:
Db 305 ILLQKLTSPDVGGND-QSQYKRLAKSTLLLPLFGVHMVFVAPPISISS---KYQILFE 360
:
QY 399 LFFNSFOGFFVSIICYNGEVQAEVKKMSRWNLSDVDWKRT-P-CGSR--CGS 450
:
Db 361 LCLGFSOGLVAVLYCYFLNSEVOCELKRRK-----SRCPTPSASRDYRVCGS 408
: :

RESULT 15
JN0616
pituitary adenylate cyclase-activating polypeptide receptor 46-5 precursor - rat
N:Alternate names: PACAP receptor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 08-Oct-1999
C:Accession: JN0616; S36768
R:Hosoya, M.; Onda, H.; Ogi, K.; Masuda, Y.; Miyamoto, Y.; Ohtaki, T.; Okazaki, H.; Arimura,
Biochem. Biophys. Res. Commun. 194, 133-143, 1993
A:Title: Molecular cloning and functional expression of rat cDNAs encoding the receptor
A:Reference number: JN0616; MUID:93326107
A:Accession: JN0616
A:Molecule type: mRNA
A:Residues: 1-467 <HOS>
A:Experimental source: brain
R:Spengler, D.; Wauber, C.; Pantaloni, C.; Holtsboer, F.; Bockaert, J.; Seeburg, P.H.; Jodanis,
Nature 365, 170-175, 1993
A:Title: Differential signal transduction by five splice variants of the PACAP receptor
A:Reference number: S36768; MUID:93382505
A:Accession: S36768
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-467 <SPE>
A:Cross-references: EMBL:D23279; NID:g404252; PID:nCAA0817.1; PID:g404253
C:Superfamily: glucagon receptor
C:Keywords: alternative splicing; glycoprotein; receptor
F:l-19/Domain: signal sequence #status predicted <SIG>
F:20-467/Product: pituitary adenylyl cyclase-activating polypeptide receptor 46-5 #stat
F:47,59,116,299,342,374/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 24.08; Score 696.5; DB 2; Length 467;

Search completed: September 21, 2001, 17:06:31
Job time: 789 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:05:47 ; Search time 13.2 seconds
(without alignments)
1403.956 Million cell updates/sec

Title: US-09-236-468a-2
Perfect score: 2907
Sequence: 1 MAWLGAHLVWGLMLGSL.....DDILMEKSRPMESNPDTG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2635	90.6	550	1 PTR2_HUMAN	P49190 homo sapien
2	2213.5	76.1	546	1 PTHR2_RAT	P70555 rattus norv
3	1397	48.1	585	1 PTHR-DIDMA	P25107 didelphis m
4	1345	46.3	585	1 PTHR-PIG	P50133 sus scrofa
5	1336.5	46.0	593	1 PTHR_HUMAN	Q03431 homo sapien
6	1331.5	45.8	591	1 PTHR_RAT	P25961 rattus norv
7	1324	45.5	591	1 PTHR_MOUSE	P41593 mus musculus
8	801	27.6	449	1 SCRC-RAT	P38111 rattus norv
9	794	27.3	445	1 SCRC-RABIT	O46502 oryctolagus
10	785	27.0	458	1 VIPR-PIG	Q28992 sus scrofa
11	784	27.0	440	1 SCRC_HUMAN	P47872 homo sapien
12	782	26.9	447	1 VIPR-CARAU	Q90308 carassius a
13	772.5	26.6	459	1 VIPR_RAT	P30083 rattus norv
14	759.5	26.1	457	1 VIPR_HUMAN	P32241 homo sapien
15	713.5	24.5	437	1 VIPS_MOUSE	P41588 mus musculus
16	708	24.4	437	1 VIPS_RAT	P35000 rattus norv
17	702	24.1	438	1 VIPS_HUMAN	P41587 homo sapien
18	685	23.6	468	1 PACR_HUMAN	P41586 homo sapien
19	677.5	23.3	496	1 PACR_MOUSE	P70205 mus musculus
20	673.5	23.0	513	1 PACR_BOVIN	Q29627 bos taurus
21	667.5	23.0	523	1 PACR_RAT	P32215 rattus norv
22	665	22.9	550	1 GLP2_RAT	Q36059 mus musculus
23	663	22.8	489	1 GLP1_MOUSE	O35659 mus musculus
24	662	22.8	462	1 GIPR_MESAU	P43218 mesocricetu
25	655	22.5	463	1 GLP1_RAT	P32301 rattus norv
26	641.5	22.1	466	1 GIPR_HUMAN	P48546 homo sapien
27	635.5	21.9	553	1 GLP2_HUMAN	O95838 homo sapien
28	630.5	21.7	423	1 GRFR_HUMAN	Q02643 homo sapien
29	628.5	21.6	463	1 GLP1_HUMAN	P43220 homo sapien
30	622.5	21.4	423	1 GRFR_PIG	P34999 sus scrofa
31	619	21.3	477	1 GLR_HUMAN	P47871 homo sapien
32	616	21.2	455	1 GIPR_RAT	P43219 rattus norv
33	607	20.9	485	1 GLR_RAT	P30082 rattus norv

RESULT 1
PTR2_HUMAN

ID	PTR2_HUMAN	STANDARD;	PRT;	550 AA.
AC	P49190;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).			
GN	PTH2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.			
RC	TISSUE=Brain;			
RX	MEDLINE=95318121; PubMed=7797535;			
RA	Usslin T.B., Gruber C., Bonner T.I.;			
RT	"Identification and functional expression of a receptor selectively			
RT	recognizing parathyroid hormone, the PTH2 receptor.";			
RL	J. Biol. Chem. 270:15455-15458(1995).			
RN	[2]			
RP	SEQUENCE OF 26-40 AND 306-550 FROM N.A.			
RX	MEDLINE=97079671; PubMed=8921382;			
RA	Usslin T.B., Modi W., Bonner T.I.;			
RT	"Assignment of the human PTH2 receptor gene (PTH2) to chromosome 2q33			
RT	by fluorescence in situ hybridization.";			
RL	Genomics 37:140-141(1996).			
CC	-1- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE			
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE			
CC	ADENYL CYCLASE.			
CC	-1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.			
CC	ALSO EXPRESSED IN THE TESTIS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U25128; AAC50157.1; -			
DR	EMBL; U47124; AAA96796.1; -			
DR	EMBL; U47129; AAC50767.1; -			
DR	EMBL; U47125; AAC50767.1; JOINED.			
DR	EMBL; U47126; AAC50767.1; JOINED.			
DR	EMBL; U47127; AAC50767.1; JOINED.			
DR	EMBL; U47128; AAC50767.1; JOINED.			
DR	GCRdb; GCR_2003; -			
DR	MIM; 601469; -			
DR	InterPro; IPR000832; -			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.			

P32082 mus musculus
O61606 mus musculus
O08893 cavia porce
Q60755 mus musculus
P32214 rattus norv
P30988 homo sapien
P79222 oryctolagus
O02644 rattus norv
Q90812 gallus gall
P25117 sus scrofa
Q60748 mus musculus
Q63118 rattus norv

ALIGNMENTS

DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.	
FT	SIGNAL 1 24 POTENTIAL.	
FT	CHAIN 25 550 PARATHYROID HORMONE RECEPTOR.	
FT	DOMAIN 27 145 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 146 169 1 (POTENTIAL).	
FT	DOMAIN 170 176 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 177 196 2 (POTENTIAL).	
FT	DOMAIN 197 237 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 238 260 3 (POTENTIAL).	
FT	DOMAIN 261 275 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 276 297 4 (POTENTIAL).	
FT	DOMAIN 298 316 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 317 337 5 (POTENTIAL).	
FT	DOMAIN 338 364 CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 365 383 6 (POTENTIAL).	
FT	DOMAIN 384 394 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 395 417 7 (POTENTIAL).	
FT	DOMAIN 418 550 CYTOPLASMIC (POTENTIAL).	
FT	CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE 550 AA; 62235 MW; 2ADD14DBA68A9BF8 CRC64;	
Query Match 90.6%; Score 2635; DB 1; Length 550;		
Best Local Similarity 91.4%; Pred. No. 2.3e-196;		
Matches 500; Conservative 6; Mismatches 29; Indels 12; Gaps 3;		
QY	1 MAWLASLHWGMLGSCLLARAQLDSGTITIEQIVLVLKAKVQCELNITAQLQEGE 60	
Db	1 MAGLGASLHWGMLGSCLLARAQLDSGTITIEQIVLVLKAKVQCELNITAQLQEGE 60	
QY	61 GNCFFPDWGLICPRGTGKISAVPCPIYDPNHHKGVAFRCNPNGTWDFPHSLNKTWA 120	
Db	61 GNCFFPDWGLICPRGTGKISAVPCPIYDPNHHKGVAFRCNPNGTWDFPHSLNKTWA 120	
QY	121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLLHCTRNHYH 180	
Db	121 NYSDCRLRFQPDISIGKQFCERLYVMYTVGYISFGSLAVAILIIGYFRRLLHCTRNHYH 180	
QY	181 MHLFVSFMLRATSIYKDRVVAHIGVKELSLIMODDPQNSIEATSVDKSQYIGCKIAV 240	
Db	181 MHLFVSFMLRATSIYKDRVVAHIGVKELSLIMODDPQNSIEATSVDKSQYIGCKIAV 240	
QY	241 VMFIYFLATNYWILVEGLYHLNLIYFAVFSOTKYLWGLILGWGPPAAFAVAWAVARAT 300	
Db	241 VMFIYFLATNYWILVEGLYHLNLIYFAVFSOTKYLWGLILGWGPPAAFAVAWAVARAT 300	
QY	301 LADARCWELSGADIKKIYQAPILAAIGLNFILNTVVRVLATKIWETNAVGHDTKQYRK 360	
Db	301 LADARCWELSGADIKKIYQAPILAAIGLNFILNTVVRVLATKIWETNAVGHDTKQYRK 360	
QY	361 LAKSTLVLLVFGVHHVIVFVCLPHSTGLGWEIRMHCELFNFNSFGFFVSIYCYNGEV 420	
Db	361 LAKSTLVLLVFGVHHVIVFVCLPHSTGLGWEIRMHCELFNFNSFGFFVSIYCYNGEV 420	
QY	421 QAEVKKWSRNWLSVDWKTTPPGCSRRCSVLTVTHSTSSQSQAANAACL---SLAK 477	
Db	421 QAEVKKWSRNWLSVDWKTTPPGCSRRCSVLTVTHSTSSQSQAANAACL---SLAK 480	
QY	478 LPRPSADSLTATSLYLAMSGVTSQRTASHTLS---TRSNKEDSGRRQDDILMEKPSRPME 534	
Db	481 IASRQPDSS-----HITLPGYVNSNEQDCLPHSFHEETKEDSGRQDDILMEKPSRPME 534	
QY	535 SNPDTEG 541	
Db	535 SNPDTEG 541	

RESULT 2

Query Match

76.1%; Score 2213.5; DB 1; Length 546;

PTH2_RAT	
ID	PTH2_RAT
AC	P70555; STANDARD; PRT; 546 AA.
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).
GN	PTH2.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_Taxid=10116;
RN	SEQUENCE FROM N.A.
RP	MEDLINE=96426194; PubMed=8828488;
RX	usdin T.B., Bonner T.I., Harta G., Mezey E.;
RA	"Distribution of parathyroid hormone-2 receptor messenger ribonucleic
RT	acid in rat.";
RL	Endocrinology 137:4285-4297(1996).
CC	FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
CC	ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC	ADENYL CYCLASE. PTHR2 MAY BE RESPONSIBLE FOR PTH EFFECTS IN A
CC	NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN
CC	PANCREATIC FUNCTION. PTHR2 PRESENCE IN NEURONS INDICATES THAT IT
CC	MAY FUNCTION AS A NEUROTRANSMITTER RECEPTOR.
CC	TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN, ARTERIAL AND
CC	CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM, IN THE HEAD OF THE
CC	EPIDIDYMS. LOWER EXPRESSION IS FOUND IN VASCULAR SMOOTH MUSCLE,
CC	EXOCRINE PANCREAS, TESTIS AND PLACENTA.
CC	EXOCRINE PANCREAS, TESTIS AND PLACENTA.
CC	SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	EMBL; U55836; AAC52849.1; -
DR	GCRDB; GCR_1413; -
DR	InterPro; IPR000832; -
DR	Pfam; PF00002; 7tm_2; 1.
DR	PRINTS; PR00249; GPCRSECRETIN.
DR	PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR	PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
DR	PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT	SIGNAL 1 24 POTENTIAL.
FT	CHAIN 25 546 PARATHYROID HORMONE RECEPTOR.
FT	DOMAIN 27 143 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 144 167 1 (POTENTIAL).
FT	DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 175 194 2 (POTENTIAL).
FT	DOMAIN 195 235 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 236 258 3 (POTENTIAL).
FT	DOMAIN 259 273 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 274 295 4 (POTENTIAL).
FT	DOMAIN 296 313 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 314 334 5 (POTENTIAL).
FT	DOMAIN 335 361 6 (POTENTIAL).
FT	TRANSMEM 362 380 7 (POTENTIAL).
FT	DOMAIN 381 391 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 392 414 7 (POTENTIAL).
FT	DOMAIN 415 546 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

Best Local Similarity 76.5%; Pred. No. 8.5e-164;		Matches 416; Conservative 37; Mismatches 82; Indels 9; Gaps 4;	
QY	1	MAWLGLSLHVMGLSCLLARAQLDSGTITIEQIVLVKAKVQCELNITTAQOEGE	60
DB	1	MPLEALPYCGLWILRLSCLVGAQLDSGTITIEQIVLVKAKVQCELNITTAQOEGE	60
QY	61	GNCFPEMDGLICWPRGTGKISAVPCPPXYIYDFNHRGVAFRHCPNPNGTWDFMHSKAKTWA	120
DB	61	GNCFPEMDGLICWPRGTAGKTSAMPSPSYVDYFNHKGVAFRHCTPNTWDFIHGSKAKTWA	120
QY	121	NYSDCLRFLOPDISKQCEFCERLYVMYTVGYSISFGSLAVAILLIYGFRLHCTRYNIH	180
DB	121	NYSDC--FLQPDINIKQCEFFENLYIYTVGYSISFGSLAVAILLIYGFRLHCTRYNIH	178
QY	181	MHLFVSMFLRATSIYFKVDRVVAHIGVKELESIMODDPONSTEATSVDSKQVIGCKIAV	240
DB	179	LHLFVSMFLRANSIFVKDRVAQHLGVEALQSLVMQGDQNFITGGSPVDSKQVIGCKIAV	238
QY	241	VMIYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFTLIGWGFPAAPFAVAWAVARAT	300
DB	239	VMIYFLATNYWILVEGLYLHNLIFVSFSDTKYLMGFTLIGWGFPAVYVAVAVARAT	298
QY	301	LADARCWELSGADIKYIQAIPILAAATGLNFIPLNTVRVLATKIWETNAVGHDRKOYRK	360
DB	299	LADTRCWELSGAD-RWYXXPILAAATGLNFIPLNTVRVLATKIWETNAVGHDRKOYRK	357
QY	361	LAKSTLVLVGVGHVYVFCVPHSTGLGWETRMHCELFNFSQGFVYSIYCYNGEV	420
DB	358	LAKSTLVLVGVGHVYVFCVPHSTGLGWETRMHCELFNFSQGFVYSIYCYNGEV	417
QY	421	QAEVKMWRNLSVDWKRTPPCGSRGCVLTVTTHSTSSQVAAAHAWCLSLAKLPR	480
DB	418	QAEVKKTWRNLSIDMKRAPCGGHRYGSLVLTVTTHSTSSQVGMGSPRLVLSKPAK	477
QY	481	SPA---DSITATSLYLAAGSVQTSRTASHTLSRNSKSGRQDDILMEKSPRPESNP	537
DB	478	TACRQIDSHVTLPGYVWSSEQDCQPS---TPETKKGHGRQEDDSPVGESSRPVAFIT	534
QY	538	DTEG 541	
DB	535	DTEG 538	
RESULT 3			
PTHR_DIDNA STANDARD; PRT; 585 AA.			
AC	P25107;		
DT	01-MAY-1992 (Rel. 22, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR		
DE	PRECURSOR (PTH/PTHr RECEPTOR).		
GN	PTHR.		
OS	Didelphis marsupialis virginiana (North American opossum).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.		
OX	NCBI_TaxID=9267;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92054592; PubMed=1658941;		
RA	Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-F., Schipani E.,		
RA	Richards J., Kolekowsky L.F. Jr., Hock J., Potts J.T. Jr.,		
RA	Kronenberg H.M., Segre G.V.,		
RT	"A G protein-linked receptor for parathyroid hormone and parathyroid		
RT	hormone-related peptide."		
RL	Science 254:1024-1026(1991).		
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR		
CC	PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS		
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL		
CC	CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER		
CC	SYSTEM.		
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		

CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M74445; AAA30979.1; -			
DR	PIR; A39286; A39286.			
DR	GCRDB; GCR_0204; -			
DR	InterPro; IPR000832; -			
DR	InterPro; IPR002170; -			
DR	Pfam; PF00002; 7tm_2; 1.			
DR	PRINTS; PR00249; GPCRSECRETIN.			
DR	PRINTS; PR00393; PTRHORMONER.			
DR	PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.			
DR	PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.			
DR	PROSITE; PS0227; G-PROTEIN_RECEP_F2_3; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.			
FT	SIGNAL 1 26 POTENTIAL.			
FT	CHAIN 27 585 PARATHYROID HORMONE/PARATHYROID HORMONE-			
FT	RELATED PEPTIDE RECEPTOR.			
FT	DOMAIN 27 185 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 186 209 1 (POTENTIAL).			
FT	DOMAIN 210 216 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 217 236 2 (POTENTIAL).			
FT	DOMAIN 237 276 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 277 300 3 (POTENTIAL).			
FT	DOMAIN 301 314 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 315 336 4 (POTENTIAL).			
FT	DOMAIN 337 355 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 356 376 5 (POTENTIAL).			
FT	DOMAIN 377 403 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 404 422 6 (POTENTIAL).			
FT	DOMAIN 423 434 EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM 435 457 7 (POTENTIAL).			
FT	DOMAIN 458 585 CYTOPLASMIC (POTENTIAL).			
FT	CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).			
FT	CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).			
SEQ	SEQUENCE 585 AA; 65963 MW; 34900384CD6DF477 CRC64;			
QY	24	AQLSDGTITIEQIVLVKAKVQCELNIT	53	
DB	24	ALVDDAVITTKESQIILLRNAQACEQLKEVLRVPELAESAADMWRSRSTKKEPAEK	83	
QY	54	--AQLEQ-----EGNCFPEMDGLICWPRGTGKISAVPCPPYIYDFNHRGVAFR	101	
DB	84	LYSQAESREVSDRSRLQDGFCLPEWDNIVCWPAGVPGKVVAVPCPDYIYDFNHRGVAFR	143	
QY	102	HCPNPTWDFMHSKAKTWAISDCFLRFLQDISIGICEFCERLYVMYTVGYSISFGSLAV	161	
DB	144	RCDNSGWSWELVPGNNRTWANSYSCVFLNETR--EREVDFRLGMITYTVGYSISGLSLTV	201	
QY	162	ATLIIGYFRLHCTRYNIHMHFLVSMFLRATSIYFKVDRVVAHIGVKELESIMQDDPQN	221	
DB	202	AVLILGYFRLHCTRYNIHMHFLVSMFLRAVSIFIKDAVLVSGVSTDEIER-ITEBELRA	260	
QY	222	STEATSVDSKQVIGCKIAVVMFYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFTL	281	
DB	261	FTEPPADKAGVGCRCVAVTVFLYITNTYIWLVEGLYLHSLIPNAFFSEKYLGMFTL	320	
QY	282	IGWGFPAFVAWAVARATLADARCWELSGADIKYIQAIPILAAATGLNFIPLNTVRVLA	341	

Db 321 FGNGLPFAVFAVAVVYVTRATIANTECHDNLSSGKKWIIQVPIILAAIVVNFILFNIIRVLA 380
Qy 342 TKIWTETNAVGHDRKQYKRLAKSTLVLVFGVHYIVFVCLPHS-FTGLGWEIRMHCELF 400
Db 381 TKURETNAGRCDFRQYKRLKSTLVLMPLFGVHYIVFMATPYTEVSGILMVQVMHYEML 440
Qy 401 FNSFGQFFVYIIYCYCNGEVOAEVKKMWSRNLSVDMKRPDPCGSRRCGSLVLTVTTH--- 457
Db 441 FNSFGQFFVYIIYCYCNGEVOAEIKKWSRWTLALDFKRRKARSGS-----STYSYGPM 493
Qy 458 -STSSOSQVAAAHAWCLSLAKLSPSPADSLTATSLYLAWSGVTSRSTASHTLSTRNKED 516
Db 494 VSTSVTNVGRGLALSLS--PRLAPGAGASANGHHQDLPYVYKHSISEN-SLPSSGPE 550
Qy 517 SGRQRDDILM-----EKPSRPMESNPDT 539
Db 551 PGTKDDGYLNGSLYEPWQGEPPPLLEERET 583
RESULT 4
PTRL_PIG
ID PTRL_PIG STANDARD; PRT; 585 AA.
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-OCT-1996 (Rel. 34, Last sequence update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHr RECEPTOR).
GN PTHr1 OR PTHr.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96305358; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor."
RL Blochm. Biophys. Acta 1307:339-347(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U18315; AAC48619.1; -
CC GCRDb; GCR1607; -
CC InterPro; IPR000832; -
CC InterPro; IPR002170; -
CC Pfam; PF00002; 7tm_2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PRINTS; PR00393; PTHHORMONER.
CC PROSITE; PS00649; G_PROTEIN_RECEPT_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEPT_F2_2; 1.
CC PROSITE; PS00227; G_PROTEIN_RECEPT_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26 POTENTIAL;
FT CHAIN 27 585 PARATHYROID HORMONE/PARATHYROID HORMONE-
FT RELATED PEPTIDE RECEPTOR.
FT DOMAIN 27 184 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 185 208 1 (POTENTIAL).
FT DOMAIN 209 215 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 216 235 2 (POTENTIAL).
FT DOMAIN 236 277 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 278 301 3 (POTENTIAL).
FT DOMAIN 302 315 4 (POTENTIAL).
FT TRANSMEM 316 337 5 (POTENTIAL).
FT DOMAIN 338 356 6 (POTENTIAL).
FT TRANSMEM 357 377 7 (POTENTIAL).
FT DOMAIN 378 404 8 (POTENTIAL).
FT TRANSMEM 405 423 9 (POTENTIAL).
FT DOMAIN 424 435 10 (POTENTIAL).
FT TRANSMEM 436 458 11 (POTENTIAL).
FT DOMAIN 459 585 12 (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 162 162 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;
Query Match 46.3%; Score 1345; DB 1; Length 585;
Best Local Similarity 52.5%; Pred. No. 1.2e-96;
Matches 259; Conservative 75; Mismatches 101; Indels 58; Gaps 7;
Qy 4 LGASLHWGWLMLGSCLL---ARAQLSDSGTITIEQIVLVKAKVQCELNITAIQLQ--- 57
Db 1 MGAARTAPGLALLCCPVLSAVALVDADDVMTKEQIFLLHRAQAQCEKRLKEVLQRP 60
Qy 58 -----EGEN-----CFPEWGLICWPRGTG 79
Db 61 DIMESDKWASAPTSKPRKEKASGLYPESGDTGSRHQRCPLPEWHILCWLPGAP 120
Qy 80 KISAVPCPPYIDFNHKGVAFRHCNPNGTWDFMHSNLKNTWANSYDCCLRFLOPDISIGKOE 139
Db 121 EVVAMPCCPDYIDFNHKGHAIRCDRNGSWELVPGHNRTWANSYDCCLRFLOPDISIGKOE 178
Qy 140 FCERLVMTVTGYSISFGSLAVAILIGYFRRLHCTRNTHHMLFVFSFMLRATPSIEVKDR 199
Db 179 VFDRLGMIVTVGYSVSLASLTAVAILAYFRRLHCTRNTHHMLFVFSFMLRATPSIEVKDR 238
Qy 200 VVIAHGVVELESIMQD-----DPQNSIEATSDVKSQYIGCKIAVWFIYFLATNYW 253
Db 239 VLYSGATLDEAERLTTEELRAIAQAFLPPVAATS-----YVGRVATFELYFLATNYW 293
Qy 254 ILVEGLYLHNLIFVAFESDTKYLWGFILGWGPPAFVAAWAVARATLADARCWELSGAD 313
Db 294 ILVEGLYLHSLIFMAFESEKKYLWGFVFGWGLPALFVAVWVSVRATLANTGCDLSSGN 353
Qy 314 IKWYQAPILAAIGLNFILPLNTVRVLATKIWETNAVGHDTKQYRKRLAKSTLVLVVFG 373
Db 354 KKWIIQVILASIVLNFILFINTVRVLATKLRNAGRCDTROQYRKLLKSTLVLMPLFG 413
Qy 374 VHYIVFVCLPHS-FTGLGWEIRMHCELFNSFGQFFVYIIYCYCNGEVOAEVKKMWSRN 432
Db 414 VHYIVFMATPYTEVSGILMVQVMHYEMLFNSFGQFFVYIIYCYCNGEVOAEIKKWSRW 473
Qy 433 LSVDMKRTPECGS 445
Db 474 LALDFKRRKARSGS 486
RESULT 5
PTRL_HUMAN
ID PTRL_HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHr RECEPTOR).
GN PTHr1 OR PTHr.
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93238641; PubMed=8386612;
RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Identical complementary deoxyribonucleic acids encode a human renal
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
RL Endocrinology 132:2157-2163(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93387403; PubMed=8397094;
RA Schneider H., Feyen J.-H., Rao Movva N.;
RT "Cloning and functional expression of a human parathyroid hormone
RL receptor.";
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95263723; PubMed=7745008;
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Juppner H.;
RT "Pseudohypoparathyroidism type 1b is not caused by mutations in the
RT coding exons of the human parathyroid hormone (PTH)/PTH-related
RT peptide receptor gene.";
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=98409426; PubMed=9737850;
RA Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;
RT "Binding domain of human parathyroid hormone receptor: from
RT conformation to function.";
RL Biochemistry 37:12737-12743(1998).
RN [6]
RP VARIANT MURK-JANSEN ARG-223
RX MEDLINE=95215874; PubMed=7701349;
RA Schipani E., Kruse K., Juppner H.;
RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type
RT metaphyseal chondrodysplasia.";
RN [7]
RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.
RX MEDLINE=96366745; PubMed=8703170;
RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,
RA Kooh S.W., Cole W.G., Juppner H.;
RT "Constitutively activated receptors for parathyroid hormone and
RT parathyroid hormone-related peptide in Jansen's metaphyseal
RT chondrodysplasia.";
RL New Engl. J. Med. 335:708-714(1996).
RN [8]
RP MUTAGENESIS OF ARG-223 AND PRO-410.
RX MEDLINE=97322091; PubMed=9178745;
RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,
RA Juppner H.;
RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate
RT signaling pathway by parathyroid hormone (PTH)/PTH-related peptide
RT receptors mutated at the two loci for Jansen's metaphyseal
RT chondrodysplasia.";
RL Mol. Endocrinol. 11:851-858(1997).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER

CC SYSTEM.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN
CC KIDNEY, BONE AND LIVER.
CC -1- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF BLOWSTRAND TYPE OF
CC CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA.
CC -1- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF MURK-JANSEN TYPE OF
CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DYSPLASIA. IT IS
CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA
CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID
CC HORMONES.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; L04308; AAA36525.1; -
CC EMBL; X68596; CAA48389.1; -
CC EMBL; U22409; AAB60657.1; -
CC EMBL; U22401; AAB60657.1; JOINED.
CC EMBL; U22402; AAB60657.1; JOINED.
CC EMBL; U22403; AAB60657.1; JOINED.
CC EMBL; U22404; AAB60657.1; JOINED.
CC EMBL; U22405; AAB60657.1; JOINED.
CC EMBL; U22406; AAB60657.1; JOINED.
CC EMBL; U22407; AAB60657.1; JOINED.
CC EMBL; U22408; AAB60657.1; JOINED.
CC EMBL; U17418; AAA56774.1; -
CC PIR; S29610; S29610.
CC PIR; A49191; A49191.
CC PDB; 1BL1; 30-MAR-99.
CC GCRDb; GCR_0205; -
CC GCRDb; GCR_0647; -
CC GCRDb; GCR_1335; -
CC GCRDb; GCR_2025; -
CC MIM; 168468; -
CC MIM; 156400; -
CC MIM; 215045; -
CC InterPro; IPR000832; -
CC InterPro; IPR002170; -
CC Pfam; PF00002; 7tm_2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PROSITE; PS00393; PTRHORMONER.
CC PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
CC PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Disease mutation; 3D-structure.
FT SIGNAL 1 26
FT CHAIN 27 593
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 593
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ	SEQUENCE	591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;	
	Query Match	45.8%; Score 1331.5; DB 1; Length 591;	
	Best Local Similarity	46.6%; Pred. No. 1.3e-95;	
	Matches 270; Conservative	86; Mismatches 136; Indels 87; Gaps 11;	
Qy	22	ARAQLSDGTTIEBQIYVLKAKVQE-----LNTAQLOEGEGN-----	62
Db	22	AAALVDADDVETKEBQIFLLHRAQACDKLLKEVLHTAANIMESDKGTWPASTSGKPRKE	81
Qy	63	-----CPEDWGLICWPRGTGKISAVCPPIYDFNHK	96
Db	82	KASGKFYPESKENKDVPYTGSRRRGRCPLPEWDNIYCWPLGAPVAVPCDYIYDFNHK	141
Qy	97	GVAFHCPNPGTWDPMSHLNKTWANSQCLRFLOPDISIGKOEFCERLYVMYTVGYSISF	156
Db	142	GHAYRCDRNCSWEVPHGHNRTWANSQCLFMTWNETR--EREVDRLGMIYTVGYSMSL	199
Qy	157	GSLAVAILIGYFRLHCTRYIHMHLFVSMRLRATSFVKDRVVVHAHIGVKELES---	213
Db	200	ASLTAVLILAYFRLHCTRYIHMHLFVSMRLRATSFVKDRVVVHAHIGVKELES---	259
Qy	214	-----IMQDDPONSIBATSVDSQYIGCKIAVVMFYFLATNYWTLVGLYLHNLIFVAF	269
Db	260	ELHIIAQVPPPPAAAAGV-----YACRCVAVTFEFLYFLATNYWTLVGLYLHSLIFMAF	314
Qy	270	FSDTKYLGWFTILGWGFPAAFAVAVARATLADARCHELSAGDITKWIYQAPILAAIGLN	329
Db	315	FSEKYLWGFITFGMLGPAFVAVVWVGRATLANTGCDLSSGHHKKWIIQVPIASVVLN	374
Qy	330	FILFNTVRLATKIWTETNAVGHDTKQYRKLAKESTLVLVLFVGHYIVFVCLPHS-FTG	388
Db	375	FILFINIIRVLATKLRETNAGRCDDTQYRKLLRSTLVLPVLFVGHYIVFVCLPHS-FTG	434
Qy	389	LGWETRMCELFNFSFQGFVFIYCYNGEVOAEVKKWMSRWNLVSVDWKTPTPCGSRRC	448
Db	435	TWQIQMHYEMLFNFSFQGFVFIYCYNGEVOAEVKKWMSRWNLVSVDWKTPTPCGSRRC	494
Qy	449	GSVLTFTVHTSSQSOVAHAHWCLSLAKLPRSPADSLTATSLYLAMSG-----VTQS	501
Db	495	SYGPMVSHTSVTVNGPRAG-----LSLPLSPRLPP---ATTNGSQLPGHAKPGAPATET	546
Qy	502	RTASHTLSTRS-----NKEDSGRQRDDILMEK	528
Db	547	ETLPVTMVPKDDGFLNGSCSLDEEASSSARPPPLQEQ	585
RESULT	7		
ID	PTRR_MOUSE	STANDARD; PRT; 591 AA.	
AC	P41593; 062119;		
DT	01-NOV-1995 (Rel. 32, Created)		
DT	01-NOV-1995 (Rel. 32, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR		
DE	PRECURSOR (PTH/PTHR RECEPTOR).		
GN	PTHR1 OR PTHR		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CBH/HEHA;		
RX	MEDLINE=95034305; PubMed=7524627;		
RA	Karperien M., van Dijk T.B., Hoeijmakers T., Cremers F.,		
RA	Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;		
RT	"Expression pattern of parathyroid hormone/parathyroid hormone		
RT	related peptide receptor mRNA in mouse postimplantation embryos		
RT	indicates involvement in multiple developmental processes."		
RL	Mech. Dev. 47:29-42(1994).		
RN	[2]		

RP	SEQUENCE FROM N.A.		
RX	STRAIN=BALB/C;		
RC	MEDLINE=94255468; PubMed=8197183;		
RA	McCuaig K.A., Clarke J.C., White J.H.;		
RT	"Molecular cloning of the gene encoding the mouse parathyroid		
RT	hormone/parathyroid hormone-related peptide receptor."		
RL	Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).		
CC	-!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR		
CC	PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS		
CC	RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL		
CC	CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER		
CC	SYSTEM.		
CC	-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; X78936; CAA55536.1; -		
DR	EMBL; L34611; AAA40011.1; -		
DR	EMBL; L34608; AAA40011.1; JOINED.		
DR	EMBL; L34607; AAA40011.1; JOINED.		
DR	EMBL; L34609; AAA40011.1; JOINED.		
DR	EMBL; L34610; AAA40011.1; JOINED.		
DR	GCRDB; GCR_1005; -		
DR	GCRDB; GCR_1614; -		
DR	MGD; MGI:97801; pthr.		
DR	InterPro; IPR000832; -		
DR	InterPro; IPR002170; -		
DR	Pfam; PF00002; 7tm_2; 1.		
DR	PRINTS; PR00249; GPCRSECRETIN.		
DR	PRINTS; PR00393; PTTHORMONER.		
DR	PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.		
DR	PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.		
DR	PROSITE; PS0227; G_PROTEIN_RECF_F2_3; 1.		
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.		
FT	SIGNAL	1 26	
FT	CHAIN	27 591	
FT	DOMAIN	27 188	
FT	TRANSMEM	189 212	
FT	DOMAIN	214 219	
FT	TRANSMEM	220 239	
FT	DOMAIN	240 282	
FT	TRANSMEM	283 306	
FT	DOMAIN	307 320	
FT	TRANSMEM	321 342	
FT	DOMAIN	343 361	
FT	TRANSMEM	362 382	
FT	DOMAIN	383 409	
FT	TRANSMEM	410 428	
FT	DOMAIN	429 440	
FT	TRANSMEM	441 463	
FT	DOMAIN	464 591	
FT	CARBOHYD	151 151	
FT	CARBOHYD	161 161	
FT	CARBOHYD	166 166	
FT	CARBOHYD	176 176	
FT	CONFLICT	27 28	
FT	CONFLICT	464 465	
FT	CONFLICT	500 501	
SQ	SEQUENCE	591 AA; 66313 MW; F7876F8D388BDDFD CRC64;	

Query Match 45.5%; Score 1324; DB 1; Length 591;
Best Local Similarity 52.4%; Pred. No. 5e-95;
Matches 250; Conservative 70; Mismatches 97; Indels 60; Gaps 6;


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DR InterPro; IPR001771; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00491; VASOACTIVEIPR.
DR PRINTS; PR01154; VIPRECEPTOR.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 31
FT CHAIN 32 458
FT
FT DOMAIN 32 143
FT TRANSMEM 144 168
FT DOMAIN 169 175
FT TRANSMEM 176 195
FT DOMAIN 196 217
FT TRANSMEM 218 241
FT DOMAIN 242 255
FT TRANSMEM 256 277
FT DOMAIN 278 293
FT TRANSMEM 294 317
FT DOMAIN 318 342
FT TRANSMEM 343 362
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FT TRANSMEM 375 394
FT DOMAIN 395 458
FT CARBOHYD 59
FT CARBOHYD 70
FT CARBOHYD 101
FT CARBOHYD 105
SQ SEQUENCE 458 AA; 51479 MW; E166E4D6B3BE1189 CRC64;

Query Match 27.0%; Score 785; DB 1; Length 458;
Best Local Similarity 37.0%; Pred. No. 1.7e-53;
Matches 182; Conservative 76; Mismatches 152; Indels 82; Gaps 18;

QY 12 GWMLGSCLLA---RAQLSDGTFIT---EEQIVLVKAKVCOELNI-TAQLQEGEGNCF 64
DB 10 GWF-----CVLAGVLACVIGPVGSWAVGLQOECEDYLMQIKVQHKCLEAQLNETSGS 65
QY 65 PEMDGLICPRGTGKISAPVCPPIYDFN-HKGV-AFRHCNPNGTWDFMHLNKTWANY 122
DB 66 KWNDLNLTCPATPRGQVGVVACLPLIFKLFSPQGLNVSRCNCTDEG-----WTP- 113
QY 123 SDCRLRLOP-----DISIGKQE-----FCERLYVMYTVGYSTSGSLAVAILIIGY 168
DB 114 -----LEPGPYPIAGMDMDKASGLDEQQTQVFNYSVKTGYTIGYSLSLAALLVATAIUSL 167
QY 169 FRRLHCTRNVIHMLFVSPMLRATSIFFKDRVVRVHAHIGVKELESIMQDDPONSIEATSV 228
DB 168 FRKLHCTRNVIHMLFISFILRATAVFIKDLALF-----DSESDHC 209
QY 229 DKSQYTGCKIAVMFYFLATNYWTLVEGLYLNHNFVAFPSDKYLMGFLIGWGFFPA 288
DB 210 SKGS-VGCKAAVVFQYCYVMANFFVLLVEGLYHLLTLLAVSFFSERKYFWGYFVGWGPS 268
QY 289 AFVAWAVARATLADARCHELSAGDIKWIYQAPILAAIGLNLFLELNTVYRVLATKIWEIN 348
DB 269 TFIWTVVRIHFEDYGCWDTTHSSLWMIKAPILASILVNFILFIRIIGILVQKLRPDP 328
QY 349 AVGHDRKQYRKLAKSTLVLVFVGHYIVFVCLPHSFTGLGWEIRMHCELFNFSGQFF 408
DB 329 -VGKSDNSPYSLAKSTLLIPLFGVHYIMFAFFPDNFKA---EVKMWVELIVGSGQVCV 384
QY 409 VSIYCYCNGEVAQAEVKMKWSRN-----LSVDWKMTTPPGCSRR---CG---SVLTFTV-- 456
DB 385 VALLYCFNGEVAQELRRKRRRHHQGVGLGWSKYQHPHSGSGSGNGDTCSTQVSMLTRVSPS 444
QY 457 --HSTSSQSOVA 466
DB 445 ARSSSFQAEVS 456
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RESULT 11
SCRC_HUMAN
ID SCRC_HUMAN STANDARD; PRT; 440 AA.
AC P47872; Q13213; Q12961;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE SECRETIN RECEPTOR PRECURSOR (SCT-R).
GN SCTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
NCBI_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA MEDLINE=95169147; PubMed=7864894;
RX Jiang S., Ulrich C.D.;
RT "Molecular cloning and functional expression of a human pancreatic
secretin receptor.";
RL Biochem. Biophys. Res. Commun. 207:883-890(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA MEDLINE=95336443; PubMed=7612008;
RX Chow B.K.-C.;
RT "Molecular cloning and functional characterization of a human
secretin receptor.";
RL Biochem. Biophys. Res. Commun. 212:204-211(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=95214632; PubMed=7700244;
RA Patel D.R., Kong Y., Sreedharan S.P.;
RT "Molecular cloning and expression of a human secretin receptor.";
RL Mol. Pharmacol. 47:467-473(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; U20178; AAC50106.1; -.
CC EMBL; U28281; AAA87556.1; -.
CC EMBL; U13989; AAA64949.1; -.
CC GCRDb; GCR_1995; -.
CC GCRDb; GCR_2016; -.
CC GCRDb; GCR_2033; -.
CC MIM; 182098; -.
CC InterPro; IPR000832; -.
CC InterPro; IPR002144; -.
CC Pfam; PF00002; 7tm_2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PRINTS; PR00490; SECRETINR.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22
FT CHAIN 23 440
FT DOMAIN 23 143
FT TRANSMEM 144 167
FT DOMAIN 168 174
```


Cypriniformes; Cyprinidae; Cyprininae; Carassius.
NCBI_TaxID=7957;
[1]
SEQUENCE FROM N.A.
MEDLINE-97190233; Pubmed-9038250;
Chow B.K.C., Yuen T.T.H., Chan K.W.;
"Molecular evolution of vertebrate VIP receptors and functional
RT characterization of a VIP receptor from goldfish *Carassius auratus*.";
RL Gen. Comp. Endocrinol. 105:176-185(1997).
CC -|- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CYCLASE.
CC
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC
CC -|- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

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or send an email to license@isb-sib.ch).

CC ENBL: U56391; AAB05459.1; --
DR GRDB; GCR_1205; --
DR InterPro; IPR000832; --
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2.1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECP_F2.2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2.3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 103 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 104 128 TRANSMEMBRANE (POTENTIAL).
FT DOMAIN 129 135 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 136 155 2 (POTENTIAL).
FT DOMAIN 156 178 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 179 202 3 (POTENTIAL).
FT DOMAIN 203 216 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 217 238 4 (POTENTIAL).
FT DOMAIN 239 255 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 257 280 5 (POTENTIAL).
FT DOMAIN 281 305 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 306 325 6 (POTENTIAL).
FT DOMAIN 326 337 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 338 357 7 (POTENTIAL).
FT DOMAIN 358 447 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 22 22 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 64 64 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 447 AA; 50959 MW; 56839E243702554C CRC64;

Query Match 26.9%; Score 782; DB 1; Length 447;
Best Local Similarity 35.0%; Pred.No.2.8e-53;
Matches 165; Conservative 82; Mismatches 137; Indels 88; Gaps 12;
ov 44 AKVOCELNITAAOLEGEGNCPEWDLICVPRGTVGKISAVPCPYIYDF--NHKGVAFR 101

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11 ARARCEKRIAGNIVSG---CAGMMDILACWFSARVGERHVIPCENIFKRFSDRHEGRLSK 67
QY 102 HCNPNGTWDQM-----HSKNTKWANYSDCLRFQLQDISIGKOFCSRLRYVMYTVG 151
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 68 TCTADG-WTEMDPMELIAYCGYNLGT-----VDDSFRRSVKIGTIG 110
QY 152 YSIFSGSLAVAILIIGYFRRLHCTRNTYHMLHFVSFMLRATSFVKDRVHVHAHIGVKELE 211
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 111 HVSLSLSLTTAIVILCKSRKLHCTRNTYHMLHFVSFILKATAVFVKDAVLY----- 161
QY 212 SLIMQDDPQNSIEATSDVKSOYIGCKIAVMFIYLATNYYIWLVEGLYHLNLIFVAFPS 271
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

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Db 162 DVIQESD--NCSTAS-----VGKAVIVFQYCI MASFFWLLVGLYLHALLAVSFFS 212
QY 272 DTKYLMGFIIGWGPFAAFAVAARATLADARWEL--SAGDIKWIYQAPILAAIGLN 329
Db 213 ERKYFWYILIGWGPTIFIMASFAKAFVNDVGCWDIIENSDFLWIIKTPILASILMN 272
QY 330 FILFLNTVRVLATKIWETNAVGHDTKQYRKLAKSTPLVLVLVFGVHYIVFVCLPHSFTGL 389
Db 273 FILFICIIIRLRQKI--NCPDIGRNESQYSLAKSTPLLLPLFGINFIIFAIPEN--I 328
QY 390 GWEIRHMCLEFNSFGFFVSIYCYCNGEVOAEVKKMSRWNL----- 433
Db 329 KTELRLVFDLLIGSFGQGVVAVLYFLNGEVOAETKRRWRHLEFLGPDTKYQHPSMG 388
QY 434 -----SVDKKTTPCGSRRCGSLVTITVTHSTSSOSQOVAAH 469
Db 389 SNGNFEISTOISMLTRCSPTRRASCTQDETSITVLGSTMGYCHQNETVKGH 440

RESULT 13
VIPR_RAT
ID VIPR_RAT STANDARD; PRT; 459 AA.
AC P30083;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPRL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=92232309; Pubmed=1314625;
RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;
RT "Functional expression and tissue distribution of a novel receptor
RT for vasoactive intestinal polypeptide.";
RL Neuron 8:811-819(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
CC (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M86835; AAA42331.1; -.
CC PIR: JH0594; JH0594.
CC GCRdb; GCR_0369; -.
CC InterPro; IPR000832; -.
CC InterPro; IPR001571; -.
CC InterPro; IPR001771; -.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PRINTS; PR00491; VASOACTIVEIPR.
CC PRINTS; PR01154; VIPRECEPTOR.
CC PROSITE; PS00649; G-PROTEIN_RECEP_F2.1; 1.
CC PROSITE; PS00650; G-PROTEIN_RECEP_F2.2; 1.
CC PROSITE; PS02227; G-PROTEIN_RECEP_F2.3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 30 POTENTIAL.
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FT CHAIN 31 459 VASOACTIVE INTESTINAL POLYPEPTIDE
FT DOMAIN 31 143 RECEPTOR 1.
FT TRANSMEM 144 168 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 169 175 1 (POTENTIAL).
FT TRANSMEM 176 195 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 196 217 2 (POTENTIAL).
FT TRANSMEM 218 241 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 242 255 3 (POTENTIAL).
FT TRANSMEM 256 277 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 278 294 4 (POTENTIAL).
FT TRANSMEM 295 318 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 319 343 5 (POTENTIAL).
FT TRANSMEM 344 363 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 364 375 6 (POTENTIAL).
FT TRANSMEM 376 395 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 396 459 7 (POTENTIAL).
FT CARBOHYD 58 59 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 69 69 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;

Query Match 26.6%; Score 772.5; DB 1; Length 459;
Best Local Similarity 36.8%; Pred. No. 1.5e-52;
Matches 172; Conservative 78; Mismatches 134; Indels 83; Gaps 17;

QY 36 EQIVLVLRKAVOCELNITLAQLEGEGNCPPEWDGLICPRGIVGKISAVPCP-----PY 89
Db 38 EYLQIETIQROQCLEE--AQLENETTGCSKMDNLTCPWTPRGOAVLDCPLIFQLFAP 95
QY 90 IYDFNHKGVAFRHCPNGTWDPMHSLINKTWANYSCLRFLOP---DISIG----- 136
Db 96 IHGYN-----ISRSCTEG-----WSQ-----LECPYHACGLNDRASSLDE 133
QY 137 --KQEFCELYVMYTVGYISFGSLAVAILIIGYFRRLHCTRTNYTHMLFVSFMLRATSI 194
Db 134 QOQTKFRVTKVTGYTIGYSLASLAVAMAILSLFRKLHCTRTNYTHMLFMSFILRATAV 193
QY 195 FVKDRVVAHIGVKELSLIMODDPQNSTEATSVDKSQVIGCKIAVVMFIYLAIFYWI 254
Db 194 FIKDMALF-----NSGEIDHCSEAS--VGCKAAVVFQYCYMANFFWL 234
QY 255 LVEGLYLHNLIEVAFPSDTKYLWGFLLIGWFPFAAFVAWAARATLADARWE--LSAGD 313
Db 235 LVEGLYLYLLAVSFESERKEYEWGILIGWVPSVFTITWTVVRIYFDFGCDWTILNSS 294
QY 314 IKWIYOAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKQYRKLAKSTPLVLVLVFG 373
Db 295 LWWIIKAPILLILVNFVLFICIRILVQKLRPPD--IGKNDSSPSYSLAKSTLLLLPLFG 353
QY 374 VHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGFFVSIYCYCNGEVOAEVKKMSRWNL 433
Db 354 IHVYMAFFPDNFEKA---QVKMVFELVWGSFGQGVVAVLYFLNGEVOAELRKRWRHNL 410
QY 434 S--VDM--KRTPPCGSRR---CG---SVLTITVT---HSTSSQSOVA 466
Db 411 QGVIGNSKSKSOHPWGSNGCATCTQVSMLTRVSPSARRSSSFQAEVS 457

RESULT 14
VIPR_HUMAN
ID VIPR_HUMAN STANDARD; PRT; 457 AA.
AC P32241; Q15871;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPRL.
OS Homo sapiens (Human).
```


RESULT 15
VIPS_MOUSE
ID VIPS_MOUSE STANDARD; PRT; 437 AA.
AC P41588; P97750;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE VASOACTIVE INTENSINAL POLYPEPTIDE RECEPTOR 2
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR)
DE (PACAP TYPE III RECEPTOR) (PACAP-R-3).
GN VIPR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=94195806; PubMed=81461174;
RA Inagaki N., Yoshida H., Mizuta M., Mizuno N., Fujii Y., Gonoi T.,
RA Miyazaki J.-I., Seino S.;
RT "Cloning and functional characterization of a third pituitary
RT adenylate cyclase-activating polypeptide receptor subtype expressed
RT in insulin-secreting cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2679-2683(1994).
RN [2]
RP SEQUENCE OF 149-407 FROM N.A.
RC STRAIN=BALB/C; TISSUE=Thymus;
RX MEDLINE=96378694; PubMed=8784257;
RA Delgado M., Martinez C., Johnson M.C., Gomariz R.P., Ganea D.;
RT "Differential expression of vasoactive intestinal peptide receptors 1
RT and 2 (VIP-R1 and VIP-R2) mRNA in murine lymphocytes.";
RL J. Neuroimmunol. 68:27-38(1996).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP AS WELL AS PACAP-38 AND -27,
CC THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH
CC ACTIVATE ADENYL CYCLASE. CAN BE COUPLED TO PHOSPHOLIPASE C.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE MIN6 CELLS,
CC AT MODERATE LEVELS IN PANCREATIC ISLETS, INSULIN-SECRETING CELLS,
CC LUNG, BRAIN, STOMACH, AND COLON, AND AT LOW LEVELS IN THE HEART.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D28132; BAA05674.1; -;
DR EMBL; S82966; -; NOT_ANNOTATED_CDS.
DR GCRDB; GCR_1028; -;
DR GCRDB; GCR_1856; -;
DR MGD; MGI:107166; Vipr2.
DR InterPro; IPR000832; -;
DR InterPro; IPR001571; -;
DR InterPro; IPR002284; -;
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00491; VASOACTIVEIPR.
DR PRINTS; PR01155; VIP2RECEPTOR.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 437 VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 2.
FT DOMAIN 23 125 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 126 150 1 (POTENTIAL).
FT DOMAIN 151 157 CYTOPLASMIC (POTENTIAL).
FT

FT	TRANSMEM	158	177	2 (POTENTIAL).
FT	DOMAIN	178	202	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	203	226	3 (POTENTIAL).
FT	DOMAIN	227	239	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	240	261	4 (POTENTIAL).
FT	DOMAIN	262	278	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	279	302	5 (POTENTIAL).
FT	DOMAIN	303	327	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	328	347	6 (POTENTIAL).
FT	DOMAIN	348	359	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	360	379	7 (POTENTIAL).
FT	DOMAIN	380	437	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	57	57	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	87	87	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	91	91	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	357	357	A -> P (IN REF. 2).
SQ	SEQUENCE	437 AA: 49473 MW: CCC870A094F9DC90	CRC64;	

Query Match 24.5%; Score 713.5; DB 1; Length 437;
Best Local Similarity 33.6%; Pred. No. 5.3e-48;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;

QY	39	VLVLKAKVOCELNITAOLOEGEGNCPP-----	-----EWDGLICWPRGTGVGKISAV	84	
DB	13	LLVRVSSIHPECFRHFLEIQEEETKCAELLSQTNORACSGVMDNITCWPRADVGTVTV	72		
QY	85	PCPPYIDF-NHKGVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFLQPDISIGKQEFCE	143		
DB	73	PCPKVFSNYSRPGNISKNCTSDG-W-----	SETFPDFIDACGYNDPE-DESKISFYIL	124	
QY	144	LYVMYVGYSGISFGSLAVAILIIGYFRRRLHCTRNHYHMLFVSMFLRATSIFVKDRVHA	203		
DB	125	VRAIYTLGYSVLSMLSTGTSIIICLFRLHCTRNHYHMLFVSMFLRATSIFVKDSVLVS	184		
QY	204	HIGVKELESILWDDPQNSIEATSDVKISQYIGCKIAVVMFTYFLATNYWILVEGLYLN	263		
DB	185	SSGL-----LRCHDQP-----	ASWVGCKLSLVFFQYICIMANFYWLLVEGLYLT	228	
QY	264	LIFVAFESDTKYLWGFILIGWGFPAFAVAARATLADARCWELSGADIK-WIYOAPI	322		
DB	229	LL-VAILPSRCFLAYLLLGWGPSVCIGAWTATRLSLEDTCGWDNDHDSIPWVIRMPI	287		
QY	323	LAAILNFIILNTVRVLATKIWETNAVGHDTKQYKRLAKSTLVLVLVFGVHYIVFVCL	382		
DB	288	LISIVVNFALFISIVRILLQKLTSPDVGND-QSQYKRLAKSTLLIPLFGVHYIMVFAAF	346		
QY	383	PHSFTGLGWEIRHMCFLFNSFGPFVSIYCYCNGCEVAEYKMKMSRWNLSDVWKRTPP	442		
DB	347	P-----IGISSTYQILFELCVGSGFGLVAVLYCYFLNSEVQCELRWR-----	390		
QY	443	CGSRRCGSLVTTVTHSTSSQSOVAAAHACLKLAKLPSPADSLTATSLYLAMSGVTQSR	502		
DB	391	-----GLCL-----	TQAGSRDYLHSHSMS-----RNGSES----	ALQIHRGSRQTQSF	429
QY	503	TASHT	507		
DB	430	LOSET	434		

Search completed: September 21, 2001, 17:08:50
Job time: 183 sec


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QY 58 DIMESDKGASASTSGPKKKEKASGLKYPSEEDKEVPGTSRRHRGRPCLPWDHILCWPL 75
Db 61 -----EGEGN-----CFPEWDGLICWPR 75
QY 76 GTVGKISAVPCPPYIYDFNHNKGVAFRHCNPGNTWDFMISLNTKNTWYNSDCLRFLOPDISI 135
Db 121 GAGGEVAVPCPDYIYDFNHNKGVAFRHCNPGNTWDFMISLNTKNTWYNSDCLRFLOPDISI 135
QY 136 GROECERLYVMYTYGYSISFGSLAVAILIIGYFRRLHCTRNYYIHMLFVSFMLRATSTF 195
Db 180 -EREVDFRLGMLTYGYSISFGSLAVAILIIGYFRRLHCTRNYYIHMLFVSFMLRATSTF 195
QY 196 VKDRVYVHAHIGVKELESLESLIMODDPONSIATSVKDSQYIGCKIAYVMFYIATNYWIL 248
Db 239 VKDAVLYSGATLDEAERLTEEBELRAIAQPPPTAAA-----GYAGCRVAVTFPLYLELA 292
QY 249 TNYWILVEGLYLHNLIFVAFSDTKYLMGFTLIGWGFPFAAFVAWAVARATLADARQWE 308
Db 293 TNYWILVEGLYLHNLIFVAFSDTKYLMGFTLIGWGFPFAAFVAWAVARATLADARQWE 308
QY 309 LSAGDIKWIYQAPILAAIAGLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVL 368
Db 353 LSSGNKKWIIQVPIIASIVLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVL 412
QY 369 VLVFGVHYIVFVCLPHS-FTGLGWEIRHMCLEFFNSFGQFFVSIYCYCNGEVAQEVKRM 427
Db 413 MPFGVHYIVFVCLPHS-FTGLGWEIRHMCLEFFNSFGQFFVSIYCYCNGEVAQEVKRM 427
QY 428 WSRNWLSDVWRTTPCGSRRCGSVLTVTHTSTSSQSOVAHAHAWCLSLAKLPRSPADSUT 487
Db 473 WSRWTLALDFKARKARSSSY-SYGMVSHTSVTVNGVRAGLGLPLSPRLPFAAAATTA 531
QY 488 ATSLYLSMGVYQTSRTASHTLTSTRNKEDSGRQDDILMEKPSRPMES 535
Db 532 TNGHPPPIGHT--KPGAPTLPTATPATAAPKDDGFLNGSCGLDEEASAPERPPALLQE 589
QY 536 NPDT 539
Db 590 EWET 593

RESULT 4
Q9PVD2 PRELIMINARY; PRT; 542 AA.
ID Q9PVD2 Q9PVD2;
AC Q9PVD2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 16, Last annotation update)
DE PARATHYROID HORMONE-RELATED PROTEIN RECEPTOR PTH3R.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Jueppner H.;
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-
RT related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is
RT Preferentially Activated by Mammalian and Fuguish Parathyroid
RT Hormone-related Peptide."
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132085; AA01286.2;
DR InterPro; IPR000832;
DR InterPro; IPR001879;
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
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SQ SEQUENCE 542 AA; 61438 MW; 08688658E2727303 CRC64;
Query Match 45.0%; Score 1307.5; DB 13; Length 542;
Best Local Similarity 48.9%; Pred. No. 9.4e-101;
Matches 260; Conservative 84; Mismatches 123; Indels 65; Gaps 10;
QY 19 CUL--ARAQLSDSGTITIEQIVLVKAKVQCELANITAOLO-EGEGNCFPEWDGLICWPR 75
Db 14 CVMGARALIDSDDVITRDEQIFLLIGARSRCERTIRAGSDVVRNENCAPEWDGLICWPR 73
QY 76 GTVGKISAVPCPPYIYDFNHNKGVAFRHCNPGNTWDFMISLNTKNTWYNSDCLRFLOPDISI 135
Db 74 GKPNOVAVVLCPEYIYDFNHNKGVAFRHCNPGNTWDFMISLNTKNTWYNSDCLRFLOPDISI 135
QY 136 GROECERLYVMYTYGYSISFGSLAVAILIIGYFRRLHCTRNYYIHMLFVSFMLRATSTF 195
Db 133 DOEEVFERLYLMYTYGYSISFGSLAVAILIIGYFRRLHCTRNYYIHMLFVSFMLRATSTF 192
QY 196 VKDRVYVHAHIGVKELESLESLIMODDPONSIATSVKDSQYIGCKIAYVMFYIATNYWIL 255
Db 193 VKDAVLYAVTNDGELED-----GAVEQRPWVGCKAAVTLFLYLLATNHYWIL 239
QY 256 VEGLYLHNLIFVAFSDTKYLMGFTLIGWGFPFAAFVAWAVARATLADARQWE 315
Db 240 VEGLYLHNLIFVAFSDTKYLMGFTLIGWGFPFAAFVAWAVARATLADARQWE 315
QY 316 WTYQAPILAAIAGLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVLFVGVH 375
Db 300 WTYQAPILAAIAGLNFILNTVRLATKIWETNAVGHDTKQYRKLAKSTLVLVLFVGVH 359
QY 376 YIVFVCLPHS-FTGLGWEIRHMCLEFFNSFGQFFVSIYCYCNGEVAQEVKRM 434
Db 360 YIMFVCLPHS-FTGLGWEIRHMCLEFFNSFGQFFVSIYCYCNGEVAQEVKRM 419
QY 435 VDWKR-----TPPGSRRCGSVLTVTHTSTSSQSOVAHAHAWCLSLAKLPRSPADSUT 488
Db 420 LDLCOKARVHSGAGSGYGGMM---SHTTQ-----PGYAPODTE 449
QY 489 TSLYLSMGVYQTSRTASHTLTSTRNKEDSGRQDDILMEKPSRPMES 540
Db 450 -SVCLSVSGA-----KGGHSLHTIGAKGSHLOHSGNL-----PGYAPODTE 490

RESULT 5
Q9R1D4 PRELIMINARY; PRT; 169 AA.
ID Q9R1D4 Q9R1D4;
AC Q9R1D4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
RT parathyroid hormone and not by human or teleost parathyroid hormone-
RT related peptide. Implications for the evolutionary conservation of
RT calcium-regulating peptide hormones."
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132083; AAD51909.1;
DR InterPro; IPR000832;
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
KW Receptor.
FT NON_TER 1 169
FT NON_TER 1 169
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SQ SEQUENCE 169 AA: 19674 MW: 748CC8231F1C69EA CRC64;
Query Match 29.5%; Score 858.5; DB 11; Length 169;
Best Local Similarity 92.9%; Pred. No. 6e-64;
Matches 158; Conservative 4; Mismatches 7; Indels 1; Gaps 1;

QY 250 NYYWILVEGLYLNHLIFVAFSDTKYLMGFIILGWGFPAAFAAFAVARATLADARCWEL 309
Db 1 NYYWILVEGLYLNHLIFVAFSDTKYLMGFIILGWGFPAAFAAFAVARATLADARCWEL 60
QY 310 SAGDIKWIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRKLAKESTLVLV 369
Db 61 SAGD-RWIIYQAPILAAIGLNFILFNTVRLATKIWETNAVGHDRKQYRKLAKESTLVLV 119
QY 370 LVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYNGE 419
Db 120 LVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFFVSIYCYNGE 169

RESULT 6
QYVHC6 PRELIMINARY; PRT; 444 AA.
AC QYVHC6;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING
DE POLYPEPTIDE RECEPTOR.
OS Rana ridibunda (laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PITUITARY;
RA Alexandre D., Anouar Y.;
RT "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue
RT distribution characteristics of both VPAC1 and VPAC2 receptors in
RT mammals.";
RL Endocrinology 0:0-0(1999).
DR EMBL; AF100644; AAD03602.1; -.
DR InterPro; IPR000832; -.
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G-PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hornr; 1.
KW Receptor.
SQ SEQUENCE 444 AA: 50955 MW: 883B25B729314C4C CRC64;

Query Match 28.0%; Score 814; DB 13; Length 444;
Best Local Similarity 36.8%; Pred. No. 9.2e-60;
Matches 168; Conservative 73; Mismatches 133; Indels 82; Gaps 12;

QY 41 VLKAKVQCELNITAQLOEE-----GNCFFPEWDLICWPRGTGKISAVPCPPY 89
Db 17 ILCVPECSIMYQIELKHPECVNHEDYFNDTAVCKRTWNTICWFSASIGEYVVLQCPY 76
QY 90 IYDFNH---KGVAFRHCNPNGTWDFMHSLNKTNWYSDCLRFQPDISTIGKOE-FCERLY 145
Db 77 FSNFTTGTGVNGVNSKNTSEG-WSEMYP-----ATYAAACGFSTNDTPTQEQTVFFGAIK 130
QY 146 VMYTVGYSISFSGSLAVAILIIGYFRRLHCTRNYIHHHLFVSFMLRATSFIVKDRVV---- 201
Db 131 TGTIGHLSLSLTAAMAILICFRKLHCTRNYIHHHLFMSFMIRAIIVFIKIDVIFESG 190
QY 202 ---HAHIGVKELESIMQDDPONSTEATSVDKSVQIGCKIAVVMFYFIATNYWILVEG 258
Db 191 ESDHCHVG-----SVGKKAANVFQYICIMANFFWLLVEG 224
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Db 65 KMDNLTCTPPTPWQVWVLDCLPFIQFSPHGYNISRNCTEEG-----WSQ- 112
QY 123 SDCLRFLOP---DISG-----KQECERLYVMYTVGYSTISFGSLAVAILIG 167
Db 113 -----LEPGYHACGLNDRASMDQOQTEFYDAVKTYTIGYSLASLLVAMAILLS 166
QY 168 YFRLHCTRNRYIHMHLFVSPMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATS 227
Db 167 LFRKLHCTRNRYIHMHLFMSFILRATAVFIKDM-----ALFNGETDHCSEAS- 213
QY 228 VDKSOYIGCKIAVVMFYFLATNYWILVEGLYHLNLIYFAVPSDTKYLGWFLILIGWGP 287
Db 214 -----VSKAAVFFQYCYMANFFWLLVEGLYHLNLIYFAVPSDTKYLGWFLILIGWGP 267
QY 288 AAFVAWAVARATLADARWE--LSAGDIKIYQAPILAAIGLNFILNTVTVRLATKIWE 346
Db 268 SVFIMTWIVRIHFEDFGCWDTIINSLLWIKGPILISILVNFILFICIRILVOKLRP 327
QY 347 TNAVGHDTKQYRKLAQSTLVLVFVGHYIVFVCLPHSFTGLGWEIRHMCHELFNFSQ 406
Db 328 PD-IGKNDSSPYSLAKSTLLIPLFGVHYVMAFFPDNFKA---QVKMVPFLVVGSGFQ 383
QY 407 FVSIYCYCNGEVOAERKMSRNLS--VDW--KRTPPCGSRR---CG---SVLTITVT 456
Db 384 FVVAIYLCFNGEVOAELRRKRRWHLQGLVWGSQSHQPMWGSNGVSCSTQVSMLTRVS 443
QY 457 ----HSTSSOSQVA 466
Db 444 PSARRSSFOAEVS 457

RESULT 8
QYJ140
ID Q9J140 PRELIMINARY; PRT; 459 AA.
AC Q9J140;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.
GN VIPRI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;
RT "Cloning and Fine Mapping of the Vasoactive Intestinal Peptide
Receptor 1 (VPAC1): A Comparative Analysis of Human, Rat and Murine
genes";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF266282; AAF7053.1; -
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEPTOR_F2_2; 1.
DR SMART; SM00008; HORMR; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52095 MW; 9D1ADF8567D4D7F CRC64;

Query Match 27.2%; Score 791.5; DB 11; Length 459;
Best Local Similarity 36.6%; Pred. No. 7.1e-58;
Matches 181; Conservative 81; Mismatches 145; Indels 87; Gaps 19;
QY 13 WMLGSCILLARA---QLSDGCTITIE---EQIVLVKAKVOCLELNTAQLOEGEGNCF 64
Db 11 WL-----CVLALACALAGPAGSRAASPHQCEYLMQIEKROOCLLEE---AQLENETTGS 64
QY 65 PEWDGLICWPRGTGKISAVPCPPYIYDFN--HKGVAFRHCNPNGTWDFMHSINKTWANY 122

Db 65 KMDNLTCTPPTPWQVWVLDCLPFIQFSPHGYNISRNCTEEG-----WSQ- 112
QY 123 SDCLRFLOP---DISG-----KQECERLYVMYTVGYSTISFGSLAVAILIG 167
Db 113 -----LEPGYHACGLNDRASMDQOQTEFYDAVKTYTIGYSLASLLVAMAILLS 166
QY 168 YFRLHCTRNRYIHMHLFVSPMLRATSIYFKDRVVAHIGVKELESIMQDDPQNSIEATS 227
Db 167 LFRKLHCTRNRYIHMHLFMSFILRATAVFIKDM-----ALFNGETDHCSEAS- 213
QY 228 VDKSOYIGCKIAVVMFYFLATNYWILVEGLYHLNLIYFAVPSDTKYLGWFLILIGWGP 287
Db 214 -----VSKAAVFFQYCYMANFFWLLVEGLYHLNLIYFAVPSDTKYLGWFLILIGWGP 267
QY 288 AAFVAWAVARATLADARWE--LSAGDIKIYQAPILAAIGLNFILNTVTVRLATKIWE 346
Db 268 SVFIMTWIVRIHFEDFGCWDTIINSLLWIKGPILISILVNFILFICIRILVOKLRP 327
QY 347 TNAVGHDTKQYRKLAQSTLVLVFVGHYIVFVCLPHSFTGLGWEIRHMCHELFNFSQ 406
Db 328 PD-IGKNDSSPYSLAKSTLLIPLFGVHYVMAFFPDNFKA---QVKMVPFLVVGSGFQ 383
QY 407 FVSIYCYCNGEVOAERKMSRNLS--VDW--KRTPPCGSRR---CG---SVLTITVT 456
Db 384 FVVAIYLCFNGEVOAELRRKRRWHLQGLVWGSQSHQPMWGSNGVSCSTQVSMLTRVS 443
QY 457 ----HSTSSOSQVA 466
Db 444 PSARRSSFOAEVS 457

RESULT 9
QYJBG2
ID Q9JBG2 PRELIMINARY; PRT; 418 AA.
AC Q9JBG2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR (FRAGMENT).
GN CVIPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kansaku N., Shimada K., Saito N., Arakawa K., Suzuki T., Matsuda Y.,
RT zadworny D.;
RT "Molecular cloning of chicken VIP receptor cDNA, tissue distribution
and chromosomal localization";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029895; BAA95164.1; -
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm.2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEPTOR_F2_2; 1.
DR SMART; SM00008; HORMR; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADCB08FF3 CRC64;

Query Match 26.8%; Score 780.5; DB 13; Length 418;
Best Local Similarity 37.1%; Pred. No. 5.3e-57;
Matches 166; Conservative 76; Mismatches 138; Indels 67; Gaps 14.
QY 32 ITTEQIVLVKAKVOCLELNTAQLOEGEGNCFPEWGLICWPRGTGKISAVPCPPYI- 90
Db 3 LEIEEE-----RSQCLAEITDQ--TSCRRQWDNITCPEAQGVVVKPCPKYFR 53


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Query Match      23.6%; Score 685.5; DB 13; Length 465;
Best Local Similarity 32.1%; Pred. No. 4.9e-49;
Matches 157; Conservative 97; Mismatches 168; Indels 67; Gaps 14;

Qy 13 WLMGSCLLARAQLDSGTTIEQIIVLVKAKYQ-CELNITAOLOEGEGNCFFEWQGLI 71
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 8 FLLGLGFMAQVASHHPYCIITKKEEACL---EKIORYEIMWNTQSG---CPGMWDNIT 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 72 CWPGRGTWKGISAVPCPPY-----IYDFNHKGVAFRHCNPNGT 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 CWMPAEVKGKVVSRCPALFSMIGSEDEMDFVDRSLGKSPENIEEQSSGTIKRNCENG- 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 109 WDFMHSUNKWANYSDCLRFLOPDISTGKQBFCERLYVWTVGYSISPGSLAVAILIY 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 W-----SEPPHYSEACDFDINTGPDQDPYYISLVKALYGTSGTSLVATTTAMVILCR 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 169 FRRLHCTPNYTHMHLFYSEMLRATSIYFKVRVWHAHIGVKELESIMODDPQNSTEATSV 228
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 FRKLHCTPNYTHMHLFVSFILRAISVFIKDEVLAE-----QDN--NCHLSTV 221
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 229 DKSYGICKAVWAFYFLATNYIWLVEGLYLNHLIEFAVFFSDTKYLWGFILIGWGPPA 288
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 222 E-----CKVWVFEHYCVMSNYFWLFIEGLYLTLLVETPEPPERYFYWYTIIGWGTP 275
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 289 AFVAAMAVRATLADARCWELUSAG-DIKWITYOAPILAAIGLNFILFLNTVRVLTAKIWE 347
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 276 ICVTIWAIVLRHLFDNLGCWDTNNNTGLWVWYIKGPVIGSIMINFLVFGVGIILIVQKL-QS 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Query Match	21.9%	Score	636:	DB	6:	Length	423:
Best Local Similarity	30.9%	Pred.	No. 5.8e-45;				
Matches	149;	Conservative	88;	Mismatches	163;	Indels	82;
Gaps							
Qy	10	VWGMLGSCLLARAQLDSDGTTIE	EQVILVLKAKVQCELNITAO	LEQEGNC	FPE	--	66
		:	: : : : : : : :				
Db	5	VWGACVL--CLL	-----GPLFI	-----VLGHV	PCDVTI	QURE	QACLQAEG 47
Qy	67	-----WDGLIC	PRGTGKISAVPCPPYIDFNHK	-GVAF	RHCNP	NGTWD	PMHS 114
		: : : : : : :					
Db	48	MPNSTGLGCPRIWDGLLC	WPTAGSGEWYSLPCPAFFS	SEP	GA	VKROCTIAG	-W----- 101
Qy	115	LNKWTANYSDCLRF	QDPDISIGKQEFERLYVMYTVGYS	ISFGS	LAVAILI	IGYFR	LRHC 174
		: : : : : : : : : : :					
Db	102	-SEPPPYEACP-VPLE	TTTEERSYFSAVRIIYTMGHSV	SAALLVAIL	ILVAL	RLHC 159	
Qy	175	TRNYTHMLFVSF	MLRATSIFFVKORVVAHIGVKE	LSLIMODD	PONSIEATS	VDKSQYI 234	
		: : : : : :					
Db	160	PRNYIHTQLFIT	FILKAAVFLKD	-----ATL	PHQENT	HCSFST	-----V 200
Qy	235	GCKIAVVMFIYFLAT	NYWILVEGLYLNHLIFVAF	FSDTKYL	WLGFI	LIGMG	FPAFVAAW 294
		: : : : : : :					
Db	201	LCKYSVATSH	EATWTFNSWLLAEAVYLTCL	LVSTLPSTR	RRVFW	LVLAAMGLP	LLFTGMW 266
Qy	295	AVARATLADARCWEL	-SAGD	LKNIYQ	YQIPILA	AGLNFL	FLNTVRVLATKIWETNAVCHD 355
		: : : : : : : :					
Db	261	VGCKLAFEDVAC	WDLDDSSPYWMIKGIVLS	VGWFG	LFLNIRIL	LRLEP	PTQGSUHL- 319

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354 TRKOYRKLANSTLVLVFGVHHVIVCVLPSTGTGWEIRMHCELFNFSGFGFVSIY 411
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
320 TQOHWRLSKSTLLPLFGIHVIEFNLPDS---AGLDTRLPLLELGLSGFGQFVAIL 376
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 414 CYCNGEVAQEVKKWMSRWNLVSDVKRTPPCGSRRCGSLVTTTTH---STSSQSOVAAAHA 470
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 377 CFLNQEVTEISRNWHGHDLLEL-----LPARVTHIKWTTPTPSHRVKVLTS 421
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 471 WC 472
   |
Db 422 AC 423

RESULT 14
Q9TUJO PRELIMINARY; PRT; 441 AA.
AC Q9TUJO;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE GROWTH HORMONE-RELEASING HORMONE RECEPTOR LONG FORM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP Masuhiro T., Tarumi O., Watanabe S., Sekikawa K.;
RA Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP Takata M., Tarumi O., Watanabe S., Sekikawa K.;
RT "Molecular cloning of bovine growth hormone-releasing hormone receptor
   cDNA."
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL: AB022597; BAA84960.1; -.
DR InterPro: IPR000832; -.
DR InterPro: IPR001879; -.
DR Pfam: PF00002; 7tm_2; 1.
DR PRINTS: PR00249; GPCRSECRETIN.
DR PROSITE: PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE: PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART: SM00008; HormR; 1.
DR Receptor.
SQ SEQUENCE 441 AA; 49251 MW; B8E11893EFC3EB88 CRC64;

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[illegible]

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Db    263 VGCKLAFEDVACWDLDDSSPYWNIIOKGPVLVSQGVNFGLNIRILLRKLEPTOGSLH- 321
Qy    354 TRKYQRKLAKSTLLVLGVFVGHYIVFVCLPSPHTGTLGWELRHMCELFNFNSFGQFFVSIY 413
      :||:|||:::||||||:|||||||:||||||:||||||:||||||:||||||:||||||:|
Db    322 TQHWRLSKSTLLILPLFGIHHVFNFLPDS---AGLDRLPLELGLSGSQGFVAIIY 378
Qy    414 CYCNGEVOAEVKMKWSRNJLS-----VDWKRTPPCGSR 446
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Db    379 CFLAQEVRTESRRWHGHDLELLPARVTHIKW--TTPSHSR 417
      :||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 15
Q9TUJ1 PRELIMINARY;          PRT;         404 AA.

AC    DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT    DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE    DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE    DE GROWTH HORMONE-RELEASING HORMONE RECEPTOR SHORT FORM.
OS    Bos taurus (Bovine).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC    Bovidae; Bovinae; Bos.
OX    NCBI_TaxID=9913;
RN    [1]
RP    SEQUENCE FROM N.A.
RA    Takata M., Tarumi O., Watanabe S., Sekikawa K.;
RT    "Molecular cloning of bovine growth hormone-releasing hormone receptor cDNA."
RL    Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR    EMBL; AB022596; BAA84959.1; -.
DR    InterPro; IPR000832; -.
DR    InterPro; IPR001879; -.
DR    Pfam; PF00002; 7tm.2; 1.
DR    PRINTS; PR00249; GPCRSECRETIN.
DR    PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR    PROSITE; PS00650; G_PROTEIN_RECP_F2_2; 1.
DR    SMART; SM00008; Hormr; 1.
KW    Receptor.
SQ    SEQUENCE   404 AA;  44868 MW;  D394FB43BECAB4AC CRC64;

Query Match       21.0%; Score 610; DB 6; Length 404;
Best Local Similarity 32.3%; Pred. No. 8e-43;
Matches 139; Conservative 79; Mismatches 149; Indels 64; Gaps

Qy    10 VWGWLMLGSCLLARAQLSDGCTITIEQIVLVLKAKVQCCELNITAIQLQGEBCNCPE--- 66
Db    5 VWGACVL--CLL-----GPLI-----VLGHVPHECDVITQLREDEQAQLQAABG 47
      :||:|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy    67 -----WDGLICWPGRGTVGKISAVPCPPYIYDENHK-GVAFRHCNPNGTWDFMHS 114
      ||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    48 MPNSTLCGPCRIWDGLLCWPAGSGEWVSLPCPAFFSHFSSEPGAVKRDCIAG-W----- 101
Qy    115 LNKTNWYSCLRLPFLDPTISIGQEFCERLYVMYTVGYISIFGSIAVALIILIIGYFRRLHC 174
      ::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    102 -SEFPFPYPACP-VPLELIITEKSYSFAVRITYTMGHVSVAALIVAILIILVLRRLHC 159
      :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy    175 TRNYIHMHVSVPMRLSTSFEYKDVRVVHAHIGWKELESIMODDPONSTEATSVDKSOYI 234
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    160 PRNYIHTOLFITILKAAAVFKD-----ATLFHQENTDHCSFSF-----V 200
      :||:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy    235 GKIAVVMFYFIATNIYYWILVEGLYLHNLIIFVAFSDPKYILWGFTILGWGEPAAFAVA 294
      ||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    201 LCKVSATSFATFNFMFWLLAAEAVALYTCLLYSTLPSTRRVFWNLVLAANGPLLTGMW 260
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Qy    295 AVARATLADARCWEL-SAGDIKIWIQAPILAAIGLNFIILFTVTRVLATKIWTNAVGHD 353
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Db    261 VGCKLAFEDVACWDLDDSSPYWNIIOKGPVLVSQGVNFGLNIRILLRKLEPTOGSLH- 319
Qy    354 TRKYQRKLAKSTLLVLGVFVGHYIVFVCLPSPHTGTLGWELRHMCELFNFNSFGQFFVSIY 413
      :||:|||:::||||||:|||||||:||||||:||||||:||||||:||||||:||||||:|

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Db 320 TQOYWRLSKSTLLIPLFGIHYVIFNLPDS---AGLDIKRPLELGLGSFQGFIVAILY 376
Qy 414 CYCNGEVOAEV 424
|: | | | |
Db 377 CFLNQEVTPV 387

Search completed: September 21, 2001, 17:09:25
Job time: 198 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 16:52:17 ; Search time 14.43 Seconds
(without alignments)
771.960 Million cell updates/sec

Title: US-09-236-468A-2
Perfect score: 2907
Sequence: 1 MAWLGLSLHVGWMLGSL.....DDILMEKPSRPMESNPDTG 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2907	100.0	541	3	US-08-468-011A-2
2	2907	100.0	541	5	PCT-US95-07085-2
3	1397	48.1	585	1	US-08-142-439A-6
4	1397	48.1	585	2	US-08-869-477-6
5	1392	47.9	585	2	US-08-142-551B-125
6	1392	47.9	585	2	US-08-468-249A-19
7	1388	47.7	515	2	US-08-468-249A-18
8	1331.5	45.8	591	2	US-08-468-249A-20
9	1331.5	45.8	593	2	US-08-468-249A-21
10	801	27.6	449	1	US-08-142-439A-5
11	801	27.6	449	2	US-08-869-477-5
12	785	27.0	458	1	US-08-112-817C-2
13	773	26.6	1324	2	US-08-811-897A-56
14	713.5	24.5	437	2	US-08-538-816A-2
15	713.5	24.5	437	2	US-09-076-651-2
16	704	24.2	431	2	US-08-538-816A-9
17	704	24.2	431	2	US-09-076-651-9
18	702.5	24.2	438	2	US-08-538-816A-1
19	702.5	24.2	438	2	US-09-076-651-1
20	696.5	24.0	448	2	US-08-811-897A-18
21	696.5	24.0	448	2	US-08-855-213-18
22	696.5	24.0	467	2	US-08-811-897A-19
23	696.5	24.0	467	2	US-08-855-213-19
24	689.5	23.7	525	2	US-08-811-897A-23
25	689.5	23.7	525	2	US-08-855-213-23
26	688.5	23.7	448	2	US-08-811-897A-16
27	688.5	23.7	448	2	US-08-855-213-16

28	688.5	23.7	485	2	US-08-811-897A-17	Sequence 17, Appl
29	688.5	23.7	485	2	US-08-855-213-17	Sequence 17, Appl
30	684.5	23.5	448	2	US-08-811-897A-22	Sequence 22, Appl
31	684.5	23.5	448	2	US-08-855-213-22	Sequence 22, Appl
32	681.5	23.4	476	2	US-08-811-897A-20	Sequence 20, Appl
33	681.5	23.4	476	2	US-08-855-213-20	Sequence 20, Appl
34	681.5	23.4	495	2	US-08-811-897A-21	Sequence 21, Appl
35	681.5	23.4	495	2	US-08-855-213-21	Sequence 21, Appl
36	675	23.2	552	2	US-08-811-897A-27	Sequence 27, Appl
37	675	23.2	552	2	US-08-855-213-27	Sequence 27, Appl
38	674.5	23.2	553	2	US-08-811-897A-25	Sequence 25, Appl
39	674.5	23.2	553	2	US-08-855-213-25	Sequence 25, Appl
40	673.5	23.2	476	2	US-08-811-897A-14	Sequence 14, Appl
41	673.5	23.2	476	2	US-08-855-213-14	Sequence 14, Appl
42	673.5	23.2	513	2	US-08-811-897A-15	Sequence 15, Appl
43	673.5	23.2	513	2	US-08-855-213-15	Sequence 15, Appl
44	672.5	23.1	553	2	US-08-811-897A-29	Sequence 29, Appl
45	672.5	23.1	553	2	US-08-855-213-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-2

Query Match 100.0% Score 2907; DB 3; Length 541;
Best Local Similarity 100.0%; Pred.No. 2.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWLGLSLHVGWMLGSLLAQLDSGTITIEQIVLVKAKVQCELNITAIQLQGE 60

Db 1 MAWLGLASLHWGMLGSCLLARAQLDSGDTITIEEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYTYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYTYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSDCRLRFQPDISIGKQECERLYVYMTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 180
Db 121 NYSDCRLRFQPDISIGKQECERLYVYMTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 180
QY 181 MHLFVSFMLRATSFYKDRVYVHAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240
Db 181 MHLFVSFMLRATSFYKDRVYVHAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240
QY 241 VMEIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFLIGWGPAAFAVAWAVARAT 300
Db 241 VMEIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFLIGWGPAAFAVAWAVARAT 300
QY 301 LADARCWELSGAGDIKWYQAPILAAIAGLNFILFLNTVVRVLAATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGAGDIKWYQAPILAAIAGLNFILFLNTVVRVLAATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540
Db 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540

RESULT 2

PCT-US95-07085-2
Sequence 2, Application PC/TUS9507085
GENERAL INFORMATION:
APPLICANT: Soppet, Daniel R
APPLICANT: Yi, Li
APPLICANT: Rosen, Craig A
APPLICANT: Ruben, Steven
TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
TITLE OF INVENTION: HLTDG74
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
STREET: Stewart & Olstein
CITY: Roseland
STATE: NJ
COUNTRY: USA
ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07085
FILING DATE: 05-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-393
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07085-2

Query Match . 100.0%; Score 2907; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. NO. 2.5e-294;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLASLHWGMLGSCLLARAQLDSGDTITIEEQIVLVKAKVQCELNITAQLQEGE 60
Db 1 MAWLGLASLHWGMLGSCLLARAQLDSGDTITIEEQIVLVKAKVQCELNITAQLQEGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYTYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYTYDFNHHKGVAFRHCNPNGTWDFMHSLNKTTWA 120
QY 121 NYSDCRLRFQPDISIGKQECERLYVYMTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 180
Db 121 NYSDCRLRFQPDISIGKQECERLYVYMTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 180
QY 181 MHLFVSFMLRATSFYKDRVYVHAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240
Db 181 MHLFVSFMLRATSFYKDRVYVHAHIGVKELESIMODDPONSTEATSVDKSQYIGCKIAV 240
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Db 241 VMEIYFLATNYWILVEGLYLNHLIFVAFSDTKYLGWFLIGWGPAAFAVAWAVARAT 300
QY 301 LADARCWELSGAGDIKWYQAPILAAIAGLNFILFLNTVVRVLAATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGAGDIKWYQAPILAAIAGLNFILFLNTVVRVLAATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420
Db 361 LAKSTLVVLVFGVHYIVFVCLPHSFTGLGWEIRMHCELFNFNSFGQFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDWKRTPPCGSRRCGSLVLTVTHTSSQSQVAAAHAWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540
Db 481 SPADSLTATSLYLAMSGVTSQRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDT 540
QY 541 G 541
Db 541 G 541

RESULT 3

US-08-142-439A-6
Sequence 6, Application US/08142439A
Patent No. 5670360
GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:

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Db 494 V$UTSVT$V$N$V$G$P$R$G$L$A$L$S$L$-P$R$L$A$P$G$A$S$A$N$G$H$Q$L$P$G$Y$V$K$H$G$S$I$E$N$-S$L$U$P$S$G$P$E 550
Qy 517 S$G$R$Q$R$D$I$L$M$-P$R$E$P$R$E$M$E$S$N$P$D$T 539
Db 551 P$G$T$K$D$D$G$Y$L$N$G$S$G$L$Y$E$P$M$V$G$E$Q$P$P$L$E$E$R$E$T 583

RESULT 4
US-08-869-477-6
; Sequence 6, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION:

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1  FILING DATE: 24-NOV-93
2  APPLICATION NUMBER: DK 398/92
3  FILING DATE: 25-MAR-92
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: PCT/EP93/00697
6  FILING DATE: 23-MAR-93
7  ATTORNEY/AGENT INFORMATION:
8  NAME: Harrington, James J.
9  REGISTRATION NUMBER: 38,711
10 REFERENCE/DOCKET NUMBER: 3756.204-US
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: 212 867 0123
13 TELEFAX: 212 867 0298
14 INFORMATION FOR SEQ ID NO: 6:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 585 amino acids
17 TYPE: amino acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: protein
21 HYPOTHETICAL: NO
22 ANTI-SENSE: NO
23 ORIGINAL SOURCE:
24 ORGANISM: Didelphis virginiana
25 US-08-869-477-6
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TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 593 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-249A-21

Query Match 45.8%; Score 1331.5; DB 2; Length 593;
Best Local Similarity 47.4%; Pred. No. 4.3e-130;
Matches 276; Conservative 80; Mismatches 135; Indels 91; Gaps 11;
QY 22 ARAQLSDGTTIEQIVLVKAKVQCELNITAQLQ----- 57
DB 22 AYALVDADDVMTKEQIFLLHRAQCEKRLAEVLQRPASIMESDKGWSASTSGKPRKD 81
QY 58 -----EGEGN-----CPPEWDGLICWPRTGKISAVPCPPYIYDFNHK 96
DB 82 KASGKLYPESEEDKEAPTGSRYGRPCLPPEWDHILCWPLGAPGEVAVPCPDYIYDFNHK 141
QY 97 GVAFRHCNPNGTWDFMHSLSKLTWANYSDCLRFQLQDISIGKQEFCEFLRYVMYTVGYSISF 156
DB 142 GHAYRCDRNGSWELVPGHNRTWANYSECVKELTNETR--EREVFDRLGMIYTVGSVSL 199
QY 157 GSLAVAILIGFRRLLHCTRTNIHMHLSFVSEMLRATSFVKDRVVAHIGVKELESLS--- 213
DB 200 ASLTAVAVLFLAYFRRLLHCTRTNIHMHLSFVSEMLRATSFVKDAVLYSGATLDEARLTEE 259
QY 214 ----TWQDDPQNSIEATSDVKSQYTGCKIATVVMFYFLATNYWILVEGLYHNLIFVAF 269
DB 260 ELRAIAQAAPPPTAAAG-----YAGCRVAVTFEFLYFLATNYWILVEGLYHLSLIFNAF 314
QY 270 RSDTKVLMGFLIGGFPAAFAVANAVARATLADARCWELSGDIKWIYQAPILAAIGLN 329
DB 315 FSEKYLWGTFTVFGGLFAVFVAVVWVSVRATLANTGNDLSSGNKKWIIQVPIIASIVLN 374
QY 330 FILFNTVRLVATKIWEYNAVGHDRKQVRLAKSTLVLVLFVGVHYIVFVCLPHS-FTG 388
DB 375 FILFINVRLVATKQRETNAGRCDFRQYRKLKSTLVLMPLFVGVHYIVFMATPYTEVSG 434
QY 389 LGWEIRMCLELFFNSFGQFFVSIYCYNGEVOAEVKKMWSRWNLSDVMKTRPPPGCSRR 448
DB 435 TLWQVQMHVEMLFNSFGQFFVSIYCYNGEVOAEVKKMWSRWNLSDVMKTRPPPGCSRR 494
QY 449 G-SVLTVTHTSSSQSOVAHAHACLSLAKLPRSPADSLTATSL-YLAMSGVTQSRT-AS 505
DB 495 SYGPMVSHTSVTNVGPRVGLG-----LPLSPRLPTATTNGHPQLPGHAKPGTAL 545
QY 506 HTLSTRS-----NKEDSGRDRDDILMEK 528
DB 546 ELETTPPAMAAPKDDGFLNGSCSLDEASGPERPPALLQE 587

RESULT 10
US-08-142-439A-5
Sequence 5, Application US/08142439A
Patent No. 5670360

GENERAL INFORMATION:
APPLICANT: Thorens, Bernard
TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
TITLE OF INVENTION: (GLP-1)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142.439A
FILING DATE: 24-NOV-93
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 398/92
FILING DATE: 25-MAR-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00697
FILING DATE: 23-MAR-93
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 3756.204-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rattus norvegicus
STRAIN: Sprague-Dawley
US-08-142-439A-5

Query Match 27.6%; Score 801; DB 1; Length 449;
Best Local Similarity 37.3%; Pred. No. 5.4e-75;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 14 LMLGCLLARQAQLSDGTTIEQIVLVKAKVQCELNITAQL-OBEGNCFPE----- 66
DB 12 LLLRLLLLITKAA-----HTGVPPRLCDVRRVLLLEBRAHCLQQLSKKKGALGPETASGE 67
QY 67 --WDLGCLWPRTGKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHSLSKLTWANY 123
DB 68 GLWDMNSCWPSAPARTVEVQCPKFLMLSNKNGSLFRNCTQDG-----WSE--- 114
QY 124 DCLRFQLQDISIG---KQEFCE-----LYVMYTVGYSISFGSLAVAILIGFRRLLH 173
DB 115 ---TPRPDLACGVNINNSFNERRHAYLLKLVMTVGVSSSLAMLLVALSILCSFRLH 171
QY 174 CTRNYIHHMLFVSFMRATSFVKDRVVAHIGVKELESIMQDDPQNSIEATSDVKSQY 233
DB 172 CTRNYIHHMLFVSFMRATSFVKDRVVAHIGVKELESIMQDDPQNSIEATSDVKSQY 212
QY 234 IGCKIATVVMFYFLATNYWILVEGLYHNLIFVAFSDTKYLMGFLIGGFPAAFAVA 293
DB 213 VGCKLVMIFFQYICINAWANLVEGLYHNLIFVAFSDTKYLMGFLIGGFPAAFAVA 272
QY 294 WAVARATLADARCWELSA-GDIKWIYQAPILAAIGLNIFLNTVRLVATKIWEYNAVGH 352
DB 273 WAITRHLENTGCWDINANASVWVIRGPVLSILNIFINILRLMKRLRTQETRGS 332
QY 353 DTRKQYRLAKSTLVLVLFVGVHYIVFVCLPHSFTGWEIRMCLELFFNSFGQFFVSI 412
DB 333 ET-NHYKRLAKSTLLIFLFGIHYIVFAFSPED-----AMEVOLFEALGSGQLVAVL 387
QY 413 YCYNGEVOAEVKKMWSRWNLSDVMKTRPPPGCSRRCGSVLTVTHTSSSQSO 464
DB 388 YCFLNGEVOLEVOKKRWHLQ-EFLPRVAFNNSFNATNGPTHSTRASTE 438

RESULT 11

US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (Glp-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
US-08-869-477-5

Query Match 27.6%; Score 801; DB 2; Length 449;
Best Local Similarity 37.3%; Pred. No. 5.4e-75;
Matches 176; Conservative 81; Mismatches 149; Indels 66; Gaps 15;

QY 14 LMLGSCLLARAQLSDGTITIEQIVLVKAKVQCELNITACL-OEGEGNCFPE-----66
DB 12 LLRLLLLTAA-----HTVGVPRLCDVRRVLEERAHCLQKSKKKGALGPETASGCE 67
QY 67 --WDGLICWPRTGVKISAVPCPPYIYDFNHK-GVAFRHCNPNGTWDFMHSLNKTNWANS 123
DB 68 GLWNNKWPSSAPARTVEVQCPELLMLSNKNGSLFRNCTQDG-----MSE-- 114
QY 124 DCLRFQPDISIG---KQEFCEP-----LYVMYTVGVSYISFGSLAVAILIYGFRRLH 173
DB 115 ---TFPRPDLACGVNINNSFNERRHAYLLKLKVMYTVGVYSSSLAMLLVALSILCSFRLH 171
QY 174 CTRNYIHMHLFVSMRLRATSIYFKVDRVVAHIGVKELESILIMODDPQNSTEATSVDKSQY 233
DB 172 CTRNYIHMHLFVSMRLRATSIYFKVDRVVAHIGVKELESILIMODDPQNSTEATSVDKSQY 233
DB 172 CTRNYIHMHLFVSMRLRATSIYFKVDRVVAHIGVKELESILIMODDPQNSTEATSVDKSQY 233

QY 234 IGCKIAVVMFIYFLATNYWILVEGLYLNLIFFVAFSDTKYLMGFIILGWGFPAAAFVAA 293
DB 213 VGCKLWMIFFQYICIMANYAWLLVEGLYLTLLAISFFSFKVKYLAQFVLWGSGSPALFVAL 272
QY 294 WAVARATLADARCWELSA-GDKWIIYQAPILAAIGLNFILFNTVRLVATKIWTNAVGH 352
DB 273 WAITRHFLENTGCDWINANASVWVIRGPIVLSILINIFFINILRILMRKLRTOETRGS 332
QY 353 DTRKQYRKLAQSLVLVLVFGVGHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGQFPVSII 412
DB 333 ET-NHYKRLAKSTLLIPLFGIHYIVFAFSPED-----AMEVQLFFELALGSGOGLVVAVL 387
QY 413 YCYNGEVAQAEYKMKMSRWNLSDMKRTPPCGSRRCGSLVTTVTHSTSSQSQ 464
DB 388 YCFLNGEVLQEVQKKRWQHLQ-EFPLRPVAFNNSFNATNGPTHSTKASTE 438

RESULT 12
US-08-112-817C-2
; Sequence 2, Application US/08112817C
; Patent No. 5573928
; GENERAL INFORMATION:
; APPLICANT: Hsiung, Hansen M.
; APPLICANT: Smith, Dennis P.
; APPLICANT: Zhang, Xing-Yue
; TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; CITY: Lilly Corporate Center
; STATE: Indianapolis
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh Iici compatible
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word for Macintosh v.5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,817C
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Richard B.
; REGISTRATION NUMBER: 35,296
; REFERENCE/DOCKET NUMBER: X-9293
; TELEPHONE: 317-276-3589
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-817C-2

Query Match 27.0%; Score 785; DB 1; Length 458;
Best Local Similarity 37.0%; Pred. No. 2.6e-73;
Matches 182; Conservative 76; Mismatches 152; Indels 82; Gaps 18;

QY 12 GWMLGSCLLA---RAQLSDGTITIT---EQIVLVKAKVQCELNIT-IAQLQEGEGNCF 64
DB 10 GWF-----CVLAGVLACVLGVPVGSWAYGLQOECDYLMIKVQHKQCELEAELETSGCS 65
QY 65 PEWDGLICWPRTGVKISAVPCPPYIYDFN-HKGV-AFRHCNPNGTWDFMHSLNKTNWANY 122
DB 66 KWDNLTCWPATPRGQVVVVLACPLIFKLFSPQTGLNVSRCNCTDEG-----WTP- 113

Qy	123	SDCLRFLQP-----DISGKQE---PCRERYVMYTVGVSYISFOSLAVAILIGY	168
Db	114	-----LEPGYPDIAGDMDDKASGLDEQQTQYFVNSVKTGTYTICYSLSLAALVATAILSL	167
Qy	169	FRRLHCTRNYIHMLHFVSFMLRATSFVFKDRVVHAHIGVKELESIMODDPONSTEATSV	228
Db	168	FRRLHCTRNYIHMLHFISFILRATAVFIKDLALF-----DSESDHC	209
Qy	229	DKSQYIGCKTAVVMFYFLATNYYWILVEGLYHLNLIFFVAFFSDTKYLMGFLIGMGPPA	288
Db	210	SKGS-VGCKAAVVLFQYCYVMANFEWLLVEGLYLHTLLAVSFFSERKYPWGYIFVGMGVP	268
Qy	289	AFVANAVARATLADARCHELSAGDTKWIYQAPILAAIGNLFIPLNTVVRVLATKIWETN	348
Db	269	TFIMVMTVVRHIFEDYGCWDTIHSSLUWIIKAPILASILVNFILTRIIGILVQQLRPDD	328
Qy	349	AVGHDTRKQYKRLAKSTFLVLVFGVHYHIVFVCLPHSETGLGWEIRMHCELFNFSQGF	408
Db	329	-VGKSDNSPYSRUAKSTLLIPLUGFVGHYIMFAFFDNFKA---EVKMWFEILVGSFGQCV	384
Qy	409	VSIYCYNGCEVAEQYKMKWMSRN-----LSVDWKRTPPCGSRR---CG---SVLTVT	456
Db	385	VAILYCFNGEVAQLRRKWRHWHQOGLGWSKYQHPSGSGSGNDTCSTQVSMILTRVSPS	444
Qy	457	--HSTSSQSQVA	466
Db	445	ARRSSSFQAEVS	456

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RESULT 13
US-08-811-897A-56
; Sequence 56, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSOYA, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABATA, Yugo
; APPLICANT: SHIMAMOTO, No. 585878710
; TITLE OF INVENTION: PACAP RECEPTER PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400

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; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-811-897A-56

Query Match 26.6%; Score 773; DB 2; Length 1324;
Best Local Similarity 36.9%; Pred. No. 2.3e-71;
Matches 174; Conservative 78; Mismatches 136; Indels 84; Gaps

QY 36 EQIVLVKAKVQCELNITAIQLQEGEGNCPEWDGLICWPGRTGVGKISAVPCP-----PY 89
Db 40 EYLQLEIEIQRQLEE--AQLNETTGCCKMDNLCTWPTTPRGAAVLDCPLIFQLFAP 97
QY 90 IYDFNHKGVAFRICNPGTWDFMHSLNKTYWANSYDCLRLQF---DISIG----- 136
Db 98 IHGYN---ISRCTPEG-----WSQ-----LEPGPHIACGLNDRASSLDE 135
QY 137 --KOEFCERLYVMYTVGYSTISFGLSAVALIIGYFRRHLHCTRNYTHMHILFVSFMLRATSI 194
Db 136 QOQTKFYNTVKTGYTIGYSLSLASLVLVAMAILSLFKLHCTRNYTHMHLFMSFILLRATAV 195
QY 195 FVKDRVVHAHIGVKELESIMQDDPONSIEATSVDKSQVIGCKIAVVMFIYFLATNYWI 254
Db 196 FIKDMALF-----NSGEIDHCSEAS-VGCKAAVVFQYCVMANFFWL 236
QY 255 LVEGLYLHNLFIFAVFFSDTKYLMGFILIGWGPFAAPAAVARATLADARCW--LSAGD 313
Db 237 LVEGLYLYTLAVSFYSERKYFMGYTILIGWGPSVEITWTVRIYFDFGCDWDTIINSS 296
QY 314 IKWIIQAPILAAITGLNFILFNTVRVLATKIWETNAVGHDTRKQYKKLAKSLTILVLVFG 373
Db 297 LWWIIIRAPILLSLVANFVLFCIIRILVQKLRPPD--IGKNDSPSYSLRAKSTLLIPLFG 355
QY 374 VHVIVFVCLPHSTFTGLGWETIRHMCLEFFNSFGQFFVSIYCYNCGEQAEVKKWNRNL 433
Db 356 IHVWTAFFPDNFKA--QVKWVFELVWCSFGQFVVAILYCFINEVQAELERRKRRHHL 412
QY 434 S--VDW--KRTPPCGSRR---CG---SVLTVT-----HSTSSQSQVAHA--HA 470
Db 413 QGVLGWSKSHQHPWGSNGATCSTQVSMLTRYSPSARRSSSFOAEVSLVNH 464

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RESULT 14
US-08-538-816A-2
: Sequence 2, Application US/08538816A
: Patent No. 5831051
: GENERAL INFORMATION:
: APPLICANT: Mojsov, Svetlana
: APPLICANT: Wei, Yang
: TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
: TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
: TITLE OF INVENTION: THEREOF
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Klauber & Jackson
: STREET: 411 Hackensack Avenue
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/538,816A
: FILING DATE: 03-OCTOBER-1995

```
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: RPACAP-3/RVIP-2
; HYPOTHETICAL: NO
; US-08-538-816A-2

Query Match 24.5%; Score 713.5; DB 2; Length 437;
Best Local Similarity 33.6%; Pred. No. 6.8e-66;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;

QY 39 VLVKAKVQCELNITAOQEGECNCP-----EWDGLICWPRGTGKISAV 84
Db 13 LLVRVSSIHPECFRHLIEQEEETKCAELLSSQENQRACSGVWDNITCRPADVGETVTV 72

QY 85 PCPPYIYDF-NHKGVAFRCHNPGNTWDFHSLNKTWANTYSDCLRFQPDISIGKQFCER 143
Db 73 PCPKVFSNFSRPGNISKNTSDG-W-----SETPDFIDACGYNDPE-DESKISFYIL 124

QY 144 LYVMYTVGYSISPGSLAVAILIIGYFRRHLCHTRNYIHMHLFVSFMLRATSIYFKDRVVA 203
Db 125 VKAIYTLGYSVLSMLSTTGSIIICLFKRLCHTRNYIHLNLFSLFMLRAISLVKDSVLVS 184

QY 204 HIGVKELESIMODDPONSTEATSVDKSQYIGCKIAVVMFIYFLATNYIWLVEGLYLNH 263
Db 185 SSGI-----LRCHDQP-----ASWVGCKLSLVFFQYCYIMANFYWLLVEGLYLHT 228

QY 264 LIFVAFESDTKYLWGFIILGWGPPAAFAVAVARATLADARCWELSAGDIK-WIYOAPI 322
Db 229 LL-VAILPPSRCFLAYLLIGWGPSVCIGAWTATRLSLEDTGCDTNDHSIPWVIRMPI 287

QY 323 LAAIGLNFILNTVRVLTATKIWETNAVGHDTKQYRKLAKSTLVLVVFGVHYIYFVCL 382
Db 288 LISIVNFAFISIVRILLOKLTSPDVGND-QSQYKRLAKSTLLIPLFGVHYMVAFAF 346

QY 383 PHSETGLGWIRHCELFNFSFGFFVSIYCYCNVEQVAKMKMSRWNLSDWKRTTP 442
Db 347 P-----IGISSTYQILFELCVSGFGLVAVVLYCFNLSEVQCELRWR-----390

QY 443 CGSRRCGSVLTWTHTSTSSOSVAAAHAWCLSLAKLPRSPADSLTATSIYLAWSGVTSR 502
Db 391 -----GLCL-----TQAGSRDYLHWSMS-----RNGSES-----ALQIHRGSRQTQSF 429

QY 503 TASHT 507
Db 430 LQSET 434

RESULT 15
US-09-076-651-2
; Sequence 2, Application US/09076651
; Patent No. 5882899
; GENERAL INFORMATION:
; APPLICANT: Mojssov, Svetlana
; APPLICANT: Wei, Yang
```

```
; TITLE OF INVENTION: RECEPTOR FOR PEPTIDE HORMONES INVOLVED
; TITLE OF INVENTION: IN ENERGY HOMEOSTASIS AND METHOD AND COMPOSITIONS FOR USE
; THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; Zip: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/076,651
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/538,816
; FILING DATE: 03-OCTOBER-1995
; APPLICATION NUMBER: US 08/437,466
; FILING DATE: 09-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-136 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: RPACAP-3/RVIP-2
; HYPOTHETICAL: NO
; US-09-076-651-2

Query Match 24.5%; Score 713.5; DB 2; Length 437;
Best Local Similarity 33.6%; Pred. No. 6.8e-66;
Matches 163; Conservative 87; Mismatches 156; Indels 79; Gaps 15;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:06:32 ; Search time 22.32 Seconds
(without alignments)
1469.426 Million cell updates/sec

Title: US-09-236-468A-2

Perfect score: 541

Sequence: 1 MAWLGLASLHWGWLMLGSL.....DDILMEKPSRMESNPDTEG 541

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 412676 seqs, 60623988 residues

Word size : 10

Total number of hits satisfying chosen parameters: 49

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	AAW12695	G-protein parathyroid
2	363	67.1	550	AAW1875	Human PTH2 seven t
3	262	48.4	550	AAW80560	Human PTH2 recepto
4	38	7.0	546	AAW80559	Rat PTH2 receptor
5	25	4.6	515	AAW27704	Opossum kidney PTH
6	25	4.6	515	AAW92275	Opossum kidney PTH
7	25	4.6	515	AAW27705	Parathyroid hormon
8	25	4.6	585	AAW73314	Opossum kidney PTH
9	25	4.6	585	AAW92276	Opossum kidney PTH
10	25	4.6	585	AAW73315	Parathyroid hormon
11	19	3.5	440	AAW80188	Amino acid sequenc

12	19	3.5	440	22	AAW71877	Human SCRC seven t
13	19	3.5	449	13	AAW30187	Secretin receptor.
14	18	3.3	324	21	AAW96985	Tethered PTH-1 rec
15	18	3.3	335	21	AAW96984	Tethered PTH-1 rec
16	18	3.3	435	21	AAW96987	Human tethered PTH
17	18	3.3	435	21	AAW07529	A mutant parathyro
18	18	3.3	446	21	AAW96983	Tethered PTH-1 rec
19	18	3.3	448	21	AAW96986	Human tethered PTH
20	18	3.3	450	21	AAW96988	Human tethered PTH
21	18	3.3	536	21	AAW96000	Zebrafish parathyr
22	18	3.3	536	21	AAW90230	Zebrafish PTH1R re
23	18	3.3	591	13	AAW27706	Rat bone PTH/pTHrP
24	18	3.3	591	17	AAW92277	Rat bone PTH/pTHrP
25	18	3.3	591	20	AAW73316	Parathyroid hormon
26	18	3.3	593	17	AAW92278	Human kidney PTH/p
27	18	3.3	593	20	AAW73317	Human Parathyroid
28	18	3.3	593	22	AAW71876	Human PTHrR seven t
29	18	3.3	614	13	AAW27707	Human kidney PTH/p
30	14	2.6	19	13	AAW27710	PTH/PTHrP receptor
31	14	2.6	19	17	AAW92281	PTH/PTHrP extracel
32	14	2.6	19	20	AAW73320	Parathyroid hormon
33	13	2.4	457	22	AAW71878	Human VIPR seven t
34	13	2.4	458	16	AAW72506	Porcine vasoactive
35	13	2.4	459	14	AAW42848	VIP receptor prote
36	12	2.2	445	21	AAW82704	Human glucose-depe
37	12	2.2	458	21	AAW51528	Human GIP receptor
38	12	2.2	466	21	AAW51526	Human GIP receptor
39	12	2.2	466	22	AAW71870	Human GIPR seven t
40	11	2.0	11	16	AAW70138	Opossum parathyroi
41	11	2.0	523	21	AAW90231	Zebrafish PTH3R re
42	11	2.0	542	21	AAW99601	Zebrafish parathyr
43	10	1.8	10	17	AAW92285	PTH/PTHrP intracel
44	10	1.8	162	15	AAW57829	Human GR C-termina
45	10	1.8	222	19	AAW68067	Human glucagon-lik
46	10	1.8	477	15	AAW50047	Human glucagon rec
47	10	1.8	477	22	AAW71872	Human GLR seven tr
48	10	1.8	550	19	AAW68066	Rat glucagon-like
49	10	1.8	553	19	AAW68065	Human glucagon-lik

ALIGNMENTS

RESULT 1
AAW12695
ID AAW12695 standard; Protein; 541 AA.
XX
AC AAW12695;
XX
DT 31-MAY-1997 (first entry)
XX
DE G-protein parathyroid hormone receptor HLTG74.
XX

KW G-protein parathyroid hormone receptor; HLTG74; parathormone; PTH;
KW calcium; signal transduction; agonist; antagonist; hypocalcaemia;
KW hyperphosphataemia; hypoparathyroidism; chronic tetany;
KW osteoporosis; hypercalcaemia; hypoparathyroidism; hypophosphataemia;
KW kidney stone; nephroliasis; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9639433-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1995; 95WO-US07085.
XX
PR 05-JUN-1995; 95WO-US07085.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Li Y, Rosen CA, Ruben SM, Soppet DR;
XX

DR WPI: 1997-043068/04.
XX N-PSDB; AAT59619.
XX Human G-protein parathyroid hormone receptor, HLTDG74 - used to
PT identify (ant)agonists, used in the treatment of hypo- or
PT hyper-calcemia, hypo- or hyper-phosphatemia, kidney stones, etc
XX
PS Claim 9; Fig 1A-E; 62pp; English.
XX A novel 7-transmembrane receptor (AAWL2695) has been identified as a
CC human G-protein parathyroid hormone (PTH) receptor. designated
CC HLTDG74.. It shows 48.2% homology to the human PTH receptor. Its
CC amino acid sequence was deduced from a cDNA clone (AAT59619) isolated
CC from a human T cell lymphoma tissue cDNA library. Recombinant
CC HLTDG74 can be produced in transfected host cells and used to
CC screen for (ant)agonist cpds. Agonists may be used to prevent or
CC treat e.g. hypocalcaemia, hyperphosphataemia, hypoparathyroidism
CC and chronic tetany by stimulating an increase in serum calcium
CC levels. Antagonists can be used to inhibit the receptor e.g. for
CC the treatment of osteoporosis, hypercalcaemia, hypoparathyroidism,
CC hypophosphataemia, kidney stone, nephroliasis.
XX
SQ Sequence 541 AA;

Query Match 100.0%; Score 541; DB 18; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWLGLSHVWGLMGLSGCLLARAQLDSGGTTTIEEQIVLVLKAKVQCELNITAQLQEGE 60
Db 1 mawlgaslhvhwglmgslgclllaraqldsdgttieeqivlvllkavqcelnitaqlqege 60
QY 61 GNCFFPMDGLICWPGRCTGCKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTWA 120
Db 61 gncfpwdglicwprgctgckisavpcppyyidfnhknkgvafrhcnpngtwdfmhslnktnwa 120
QY 121 NYSDCURFLQPDISIGKQBFCEFLRYVMYTVGYSGISFGLSLAVAILIIGYFRRLHCTRNYIH 180
Db 121 nysdcrlfqpdisigkqbfceerlymytvgyysifsgslavailiigyfrlhcrtnyih 180
QY 181 MHLFVSFMLRATSFVKDRVVAHIGVKELESIMQDDPQNSIEATSVDKSQYIGCKIAV 240
Db 181 mhlvfmrlratsfvdrrvvhahigvkeleslmqddbpqnsieatsvdksgyigckiaav 240
QY 241 VMFIPLATNYWILVEGLYLNHLNIFVAFSDTKYLMGFIILGWGFPAAFAVAWAVARAT 300
Db 241 vmfiylatnywylveglylnhlifvafsdtkylmgfllgwfgfpaaafvaawavarat 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTRKQYRK 360
Db 301 ladarcwelsagdikwiypapilaaiglnflflntvrvlatkietnavghdtrkqyrk 360
QY 361 LAKSTLVLVIVGVHVIVFVCLPHSFSTGLGWETRMHCELFENSGQFFVSIYCYCNGEV 420
Db 361 lakstlvlvivgvhvvivfclphsfstglgwetrmhcelfensgqffvsiycycngev 420
QY 421 QAEVKKMWSRWNLSDVWKRTPTPCGSRRCGSLVTTVTHSTSSQVAAAHAWCISLAKLPR 480
Db 421 qaevkkmwswrnlsvdwrtpptpcgsrrcgsylvttvthstssqvaahawcislaklpr 480
QY 481 SPADSLTATSLYLAMSGVGTQSTASHTLSTRNKEDSGRQRDILMEKPSRPMESNPDE 540
Db 481 spadsltatslylamsgvgtqstashtlstrnkedsgrqrddilmekpsrmpesnpdte 540

QY 541 G 541
Db 541 g 541

RESULT 2
AAB71875
ID AAB71875 standard; Protein; 550 AA.

XX AAB71875;
AC
XX
DT 03-MAY-2001 (first entry)
XX
DE Human PTR2 seven transmembrane domain.
XX
KW Human; PTR2; parathyroid hormone receptor; hl5571; immunomodulatory;
KW vascular; hepatic; antiasthma; antimicrobial; antiinflammatory;
KW immunosuppressive; gene therapy; vaccine; G-protein coupled receptor;
KW GPCR; liver fibrosis; respiratory disorder; infection;
KW chronic inflammatory disease; organ-specific autoimmunity;
KW graft rejection; cystic fibrosis.
OS
XX Homo sapiens.
PN WO200109328-A1.
XX
PD 08-FEB-2001.
XX
PF 03-AUG-2000; 2000WO-US21278.
XX
PR 03-AUG-1999; 99US-0146916.
PR 29-FEB-2000; 2000US-0515781.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR, Lloyd C, Welch NS;
XX
DR WPI: 2001-138653/14.
XX
PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
XX
PS Disclosure: Fig 2; 145pp; English.
XX
CC The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated hl5571. hl5571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.
XX
SQ Sequence 550 AA;

Query Match 67.1%; Score 363; DB 22; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHVWGLMGLSGCLLARAQLDSGGTTTIEEQIVLVLKAKVQCELNITAQLQEGEGNC 63
Db 4 lgaslhvhwglmgslgclllaraqldsdgttieeqivlvllkavqcelnitaqlqegecnc 63
QY 64 FPEWDLICWPRGTGCKISAVPCPPYIYDFNHNKGVAFRHCNPNGTWDFMHSLNKTWANSY 123
Db 64 fpewdglcwrpgrtgckisavpcppyyidfnhknkgvafrhcnpngtwdfmhslnktwansy 123
QY 124 DCLRFLQPDISIGKQBFCEFLRYVMYTVGYSGISFGLSLAVAILIIGYFRRLHCTRNYIHML 183
Db 124 dclrlfqpdisigkqbfceflrymytvgyysifsgslavailiigyfrlhcrtnyihml 183

QY 184 FVSPMLRATSIFFKDRVVHAGHIGVKELESIMQDDPQNSIEATSVDKSIQYIGCKIAVVMF 243
DB 184 fvsfmlratsifvkdrrvvhahigvkeleslmqddpqnsieatsvdksqyigckiaavmf 243
QY 244 IYFLATNYWTLVSGLYLHNLIFVAFSDTKYLMGFLIIGHGFFPAFVAANAVARATLAD 303
DB 244 IYFLATNYWTLVSGLYLHNLIFVAFSDTKYLMGFLIIGHGFFPAFVAANAVARATLAD 303
QY 304 ARCWELSGADIKWYIQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLA 363
DB 304 arcwelsagdikwyiqapilaaiglnfilntvrlatkiwetnavghdrkqyrklak 363
QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423
DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423
QY 424 VKMWSRWNLSDVDMKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467
DB 424 vkwmwsrwnlsdvdmkrtppcgrrcgsavlvtvthstssqsvaa 467

RESULT 3
AAB80560
ID AAB80560 standard; Protein: 550 AA.
XX
AC AAB80560;
XX
DT 26-APR-2001 (first entry)
XX
DE Human PTH2 receptor amino acid sequence.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;
KW cytotatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Homo sapiens.
XX
PN W0200077042-A2.
XX
PD 21-DEC-2000.
XX
XX 15-JUN-2000; 2000WO-US16776.
XX
XX 15-JUN-1999; 9905-0139335.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Usdin TB, Hoare SRJ;
XX
XX WPI; 2001-122833/13.
XX
XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
XX
XX Example 4; Fig I; 106pp; English.
XX
CC The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepression,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiatic, cytotatic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or

CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. The present
CC sequence represents a PTH2 receptor which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 550 AA;
XX
Query Match 48.4%; Score 262; DB 22; Length 550;
Best Local Similarity 99.6%; Pred. No. 1e-259;
Matches 462; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4 LGASLHVWGVMMLGSCLLARAGLSDGTITIEQIVLVKAKVQCELNITAGLQEGNCG 63
DB 4 Lgaslhvvgwmlgscllaraqlsdgtitieeqivlvkakvqcelnitaqlqegnc 63
QY 64 FPEWDGLICWPRGTIVGKISAVPCPPYIYDFNHKGVAFRHCPNPGTWDPHSLNKTWANS 123
DB 64 fpewdglcwpgrgtvgkisavpcppyiydfnhkgvafhrhcnpgntwdfmhslnktwans 123
QY 124 DCLRFLOPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGVFRRLHCTRNYIHML 183
DB 124 dclrflopdisigkqecerlyvmytvgyisfsgslavailiigvfrlhrctnryihmhl 183
QY 184 FVSPMLRATSIFFKDRVVHAGHIGVKELESIMQDDPQNSIEATSVDKSIQYIGCKIAVVMF 243
DB 184 fvsfmlratsifvkdrrvvhahigvkeleslmqddpqnsieatsvdksqyigckiaavmf 243
QY 244 IYFLATNYWTLVSGLYLHNLIFVAFSDTKYLMGFLIIGHGFFPAFVAANAVARATLAD 303
DB 244 IYFLATNYWTLVSGLYLHNLIFVAFSDTKYLMGFLIIGHGFFPAFVAANAVARATLAD 303
QY 304 ARCWELSGADIKWYIQAPILAAIGLNFILNTVRLATKIWETNAVGHDRKQYRKLA 363
DB 304 arcwelsagdikwyiqapilaaiglnfilntvrlatkiwetnavghdrkqyrklak 363
QY 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423
DB 364 STLVLVLVFGVHYIVFVCLPHSFTGLGWEIRHMCLEFNSFGQFVSIYCYCNGEVOAE 423
QY 424 VKMWSRWNLSDVDMKRTPPCGSRRCGSLVTVTHTSTSSQSOVAA 467
DB 424 vkwmwsrwnlsdvdmkrtppcgrrcgsavlvtvthstssqsvaa 467

RESULT 4
AAB80559
ID AAB80559 standard; Protein: 546 AA.
XX
AC AAB80559;
XX
DT 26-APR-2001 (first entry)
XX
DE Rat PTH2 receptor amino acid sequence.
XX
KW Tuberinfundibular peptide of 39 residues; TIP39; PTH2 receptor ligand;
KW parathyroid hormone; parathyroid hormone receptor; anorectic; nootropic;
KW PTH2 receptor binding activity; antidepression; neuroleptic; analgesic;
KW antimigraine; antidiabetic; osteopathic; hypertensive; cardiatic;
KW cytotatic; antiasthmatic; neuroprotective; PTH receptor antagonist;
KW obesity; eating disorder; metabolic disorder; mental disorder;
KW depression; schizophrenia; dementia; acute pain; chronic pain; migraine;
KW headache; diabetes; osteoporosis; hypercalcaemia; calcium metabolism;
KW hypertension; congestive heart failure; tumour; asthma; emphysema;
KW restrictive lung disease; demyelinating condition; multiple sclerosis;
KW leukodystrophy.
XX
OS Rattus sp.

```
XX WO200077042-A2.
PN
XX
XX 21-DEC-2000.
PD
XX
XX 15-JUN-2000; 2000WO-US16776.
PF
XX
XX 15-JUN-1999; 99US-0193335.
PR
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Usdin TB, Hoare SRJ;
PI
XX
XX WPI: 2001-122833/13.
DR
XX
XX New parathyroid hormone type 2 or 1 receptor ligand, useful for
PT treating e.g. migraine or headaches, hypertension, obesity and other
PT eating or metabolic disorders, mental disorders and osteoporosis -
PT
XX
XX Example 4; Fig I; 106pp; English.
PS
XX
XX The present invention describes an isolated or purified peptide (I) that
CC is a parathyroid hormone type 2 (PTH2) receptor ligand (Ia) or PTH1
CC receptor ligand (Ib). (I) has anorectic, neuroleptic, antidepressant,
CC nootropic, analgesic, antimigraine, antidiabetic, osteopathic,
CC hypertensive, cardiac, cytotactic, antiasthmatic and neuroprotective
CC activities, and is an PTH receptor antagonist. The peptide is useful in
CC the treatment of a disorder mediated by binding a PTH2 or PTH1 receptor.
CC The PTH2 receptor binding activity may be used in treating obesity or
CC other eating or metabolic disorders, mental disorders (e.g. depression,
CC schizophrenia and dementia), acute or chronic pain, migraine or
CC headaches, diabetes and other metabolic disorders, osteoporosis,
CC hypercalcaemia and other disorders affecting calcium metabolism,
CC hypertension, congestive heart failure and control of tumour growth,
CC asthma, emphysema or other restrictive lung diseases, and demyelinating
CC conditions such as multiple sclerosis and leukodystrophies. The present
CC sequence represents a PTH2 receptor which is used in the
CC exemplification of the present invention.
XX
XX Sequence 546 AA;
SQ

Query Match 7.0%; Score 38; DB 22; Length 546;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WTYQAPILAAIGLNFILFNTVRLATKIWTETNAVGH 353
DB 313 WYQAPILAAIGLNFILFNTVRLATKIWTETNAVGH 350

RESULT 5
AAR27704
ID AAR27704 standard; Protein; 515 AA.
XX
XX AAR27704;
AC
XX
XX 16-MAR-1993 (first entry)
DT
XX
XX Opossum kidney PTH/PTHrP receptor prep. from clone OK-H.
DE
XX
XX Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia.
XX
XX Didelphis virginiana.
OS
XX
XX WO9217602-A.
PN
XX
XX 15-OCT-1992.
PD
XX
XX 06-APR-1992; 92WO-US02821.
PF
XX
XX 05-APR-1991; 91US-0681702.
PR
```

```
PR 06-APR-1992; 92US-0864475.
XX
XX (GEHO ) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
PA
XX
XX Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
PI
XX
XX WPI: 1992-366271/44.
DR
XX
XX N-PSDB; AAQ29604.
DR
XX
XX New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
PT
XX
XX Disclosure; Fig 1; 91pp; English.
PS
XX
XX The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-H, isolated from opossum kidney (OK) cells. The protein
CC may be used in a therapeutic compsn. to inhibit activation of PTH or
CC PTHrP and thus reduce the level of calcium in the blood. Cpd.
CC capable of competing with PTH or PTHrP for binding can be identified
CC using the protein prod. and DNAs homologous to PTH DNA can be
CC identified using fragments of the clone as probes. The protein
CC may be used for the prodn. of antibodies useful for the treatment,
CC classification, prognosis and/or treatment of disorders related to
CC the interaction between a cell receptor and a ligand such as in
CC hypercalcaemia. See also AAR27705-16.
XX
XX Sequence 515 AA;
SQ

Query Match 4.6%; Score 25; DB 13; Length 515;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFVSFMLRA 191
DB 207 GYFRLHCTRNVIHMHFVSFMLRA 231

RESULT 6
AAR92275
ID AAR92275 standard; Protein; 515 AA.
XX
XX AAR92275;
AC
XX
XX 18-MAY-1996 (first entry)
DT
XX
XX Opossum kidney PTH/PTHrP receptor.
DE
XX
XX Parathyroid hormone; receptor; parathormone; PTH;
KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX
XX Didelphis virginiana.
OS
XX
XX US5494806-A.
PN
XX
XX 27-FEB-1996.
PD
XX
XX 05-APR-1991; 91US-0681702.
PF
XX
XX 06-APR-1992; 92US-0864475.
PR
XX
XX 05-APR-1991; 91US-0681702.
PR
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX
XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
PI
XX
XX WPI: 1996-139028/14.
DR
XX
XX N-PSDB; AAT15945.
DR
```


XX DNA encoding vertebrate parathyroid hormone receptor - useful for
PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
PT cancer etc.
XX
PS Claim 1; Fig 1A-1E; 64pp; English.
XX
CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
CC receptors (AAR92275 and AAR92776) are encoded by cDNA clones OK-H
CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
CC separate genes or of a laboratory artifact. The receptor induces an
CC increase in intracellular cAMP and calcium when challenged with PTH or
CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
CC Host cells expressing the receptor can be used for diagnostic
CC measurement of PTH serum levels.
XX
SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 17; Length 515;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNYYIMHFLVSPMLRA 191
|||||
DB 207 gyfrlhcetnyimhflvsvmlra 231
|||||

RESULT 7
AAR73314
ID AAW73314 standard; Protein; 515 AA.
XX
AC AAW73314;
XX
DT 08-FEB-1999 (first entry)
XX
DE Parathyroid hormone receptor OK-H.
XX
KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
KW PTH-related hypercalcaemia; opossum.
XX
OS Didelphis virginiana.
XX
PN US5840853-A.
XX
PD 24-NOV-1998.
XX
PF 06-JUN-1995; 95US-0471494.
XX
PR 06-APR-1992; 92US-0864475.
PR 03-APR-1991; 91US-0681702.
PR 06-JUN-1995; 95US-0471494.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
PI Schipani E, Segre GV;
XX
DR N-PSDB; AAV08388.
XX
XX Antibody to parathyroid hormone receptor - for diagnostic or
PT therapeutic use
PT
PS Claim 6; Fig 1; 63pp; English.
XX
CC This sequence represents the opossum parathyroid hormone (PTH) receptor
CC OK-H, which is targeted by the antibody of the invention. The antibody
CC of the invention is immunoreactive with naturally occurring human, rat or
CC opossum PTH receptor. The antibody is useful for treating disorders

CC characterised by overstimulation of PTH receptors by their ligand and for
CC the diagnosis of PTH-related hypercalcaemia.
XX
SQ Sequence 515 AA;

Query Match 4.6%; Score 25; DB 20; Length 515;
Best Local Similarity 100.0%; Pred. No. 6.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLHCTRNYYIMHFLVSPMLRA 191
|||||
DB 207 gyfrlhcetnyimhflvsvmlra 231
|||||

RESULT 8
AAR27705
ID AAR27705 standard; Protein; 585 AA.
XX
AC AAR27705;
XX
DT 16-MAR-1993 (first entry)
XX
DE Opossum kidney PTH/PTHrP receptor prod. from clone OK-O.
XX
KW Parathyroid hormone; related protein; calcium; antagonist;
KW antibodies; hypercalcaemia.
XX
OS Didelphis virginiana.
XX
PN WO9217602-A.
XX
PD 15-OCT-1992.
XX
PF 06-APR-1992; 92WO-US02821.
XX
PR 05-APR-1991; 91US-0681702.
PR 06-APR-1992; 92US-0864475.
XX
PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
XX
PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;
PI Segre GV;
XX
DR WPI; 1992-366271/44.
DR N-PSDB; AAQ29605.
XX
PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
PT and treatment of tumours
XX
PS Disclosure; Fig 2; 91pp; English.
XX
CC The parathyroid hormone/parathyroid hormone related protein (PTH/PTHrP)
CC receptor protein sequence was deduced from the DNA sequence of the
CC clone OK-O, isolated from opossum kidney (OK) cells. The clone OK-O
CC is identical to the OK-H clone except at the C-terminal tail as OK-O
CC encodes a 585 amino acid protein, OK-H encodes one of 515 amino acids.
CC The difference is attributed to a single nucleotide deleted in the OK-H
CC sequence causing a frame shift and an earlier stop codon. It is not
CC known whether OK-O and OK-H represent prods. of two separate genes or
CC a laboratory artifact. The protein may be used in a therapeutic
CC compsn. to inhibit activation of PTH or PTHrP and thus reduce the
CC level of calcium in the blood. Cpts. capable of competing with PTH
CC or PTHrP for binding can be identified using the protein prod. and
CC DNAs homologous to PTH DNA can be identified using fragments of the
CC clone as probes. The sequence may be used for the prodn. of antibodies
CC useful for the treatment, classification, prognosis and/or treatment of
CC disorders related to the interaction between a cell receptor and a
CC ligand such as in hypercalcaemia. See also AAR27704-16.
XX
SQ Sequence 585 AA;

```
Query Match      4.6%; Score 25; DB 13; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhctrnyihmhlfvsmflra 231

RESULT 9
AAR92276
ID AAR92276 standard; Protein; 585 AA.
XX AC AAR92276;
XX XX 18-MAY-1996 (first entry)
XX DE Opossum kidney PTH/PTHrP receptor.
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer; opossum.
XX OS Didelphis virginiana.
XX XX US5494806-A.
XX PN 27-FEB-1996.
XX PD 05-APR-1991; 91US-0681702.
XX PF 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PT (GEO ) GEN HOSPITAL CORP.
XX PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX XX WPI; 1996-139028/14.
XX DR N-PSDB; AAT15946.
XX XX DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX PS Claim 1; Fig 2A-2E; 64pp; English.
XX CC Parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP)
XX CC receptors (AAR92275 and AAR92276) are encoded by cDNA clones OK-H
XX CC (AAT15945) and OK-O (AAT15946), respectively, isolated from an opossum
XX CC kidney (OK) cell cDNA library. OK-H and OK-O may be the products of 2
XX CC separate genes or of a laboratory artifact. The receptor induces an
XX CC increase in intracellular cAMP and calcium when challenged with PTH or
XX CC PTHrP. Recombinant receptors can be produced in vector/host cell systems
XX CC and used in the treatment, diagnosis or prognosis of e.g. hypercalcaemia
XX CC and hypocalcaemia, to screen for (ant)agonists and to raise antibodies.
XX CC Host cells expressing the receptor can be used for diagnostic
XX CC measurement of PTH serum levels.
XX SQ Sequence 585 AA;
```

```
Query Match      4.6%; Score 25; DB 17; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhctrnyihmhlfvsmflra 231
```

```
RESULT 10
AAW73315
ID AAW73315 standard; Protein; 585 AA.
XX AC AAW73315;
XX XX 08-FEB-1999 (first entry)
XX DE Parathyroid hormone receptor OK-O.
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; opossum.
XX OS Didelphis virginiana.
XX XX US5840853-A.
XX PN 24-NOV-1998.
XX PD 06-JUN-1995; 95US-0471494.
XX PF 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX XX (GEO ) GEN HOSPITAL CORP.
XX PA Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX XX WPI; 1999-034124/03.
XX DR N-PSDB; AAV08389.
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX XX Claim 6; Fig 2; 63pp; English.
XX CC This sequence represents the opossum parathyroid hormone (PTH) receptor
XX CC OK-O, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
XX SQ Sequence 585 AA;

Query Match      4.6%; Score 25; DB 20; Length 585;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNVIHMHFLVFSFMLRA 191
    |||||||
Db 207 gyfrrlhctrnyihmhlfvsmflra 231

RESULT 11
AAB08188
ID AAB08188 standard; Protein; 440 AA.
XX AC AAB08188;
XX XX 04-DEC-2000 (first entry)
XX DE Amino acid sequence of rat secretin receptor polypeptide.
XX KW Secretin; gastrointestinal hormone; pancreatic fluid; S cell;
XX KW pancreatic cell growth; pancreatic beta cell; pancreatic islet;
XX KW insulin production; glucose metabolism; insulin resistance;
XX KW glucose intolerance; hyperglycemia; hyperinsulinemia; obesity;
XX KW hyperlipidemia; hyperproteinemia; Type II diabetes mellitus;
XX KW secretin receptor.
```

XX OS Rattus sp.
 XX PN WO200047721-A2.
 XX PD 17-AUG-2000.
 XX PF 10-FEB-2000; 2000WO-US03422.
 XX PR 10-FEB-1999; 99US-0119575.
 XX PA (ONTO-) ONTOGENY INC.
 XX PI Kagan D, Pang K;
 XX DR WPI; 2000-515058/46.
 XX DR N-PSDB; AAA63813.
 XX PT Secretin therapeutic is used to modulate the growth state of pancreatic
 PT cells to provide treatment for diabetes through modification of glucose
 PT metabolism -
 XX PS Disclosure; Page 88-90; 90pp; English.
 XX CC The present sequence represents a rat secretin receptor polypeptide.
 CC Secretin is a gastrointestinal hormone that stimulates the secretion of
 CC bicarbonate-rich pancreatic fluid. Secretin is produced by specific
 CC endocrine cells (S cells) located in the mucosa of the proximal small
 CC intestine. Secretion of secretin is stimulated by the presence of either
 CC acidic pH or fatty acids in the duodenum. The specification describes
 CC a method for modulating the growth state of pancreatic cells. The method
 CC comprises contacting the cells with a secretin therapeutic or prodrug
 CC form of secretin. Secretin is used to modulate the growth state of
 CC pancreatic cells, in particular to promote the proliferation of
 CC pancreatic cells, generate functional pancreatic beta cells from
 CC pancreatic islets or cells, promote insulin production in a pancreatic
 CC islet or cell, antagonize insulin inhibition of secretin response in
 CC secretin-responsive cells, modify glucose metabolism in an animal to
 CC treat a disease associated with altered glucose metabolism e.g. insulin
 CC resistance, glucose intolerance or non-responsiveness, hyperglycemia,
 CC hyperinsulinemia, obesity, hyperlipidemia, hyperproteinemia or Type II
 CC diabetes mellitus (NIDDM).
 XX SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 21; Length 440;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNTHMHLFVSF 187
 |||||
 Db 167 frrlhctnrnyhmlhlfvsf 185

RESULT 12
 AAB71877
 ID AAB71877 standard; Protein; 440 AA.
 XX AC AAB71877;
 XX DT 03-MAY-2001 (first entry)
 XX DE Human SCRC seven transmembrane domain.
 XX KW Human; SCRC; secretin receptor; h15571; immunomodulatory; vascular;
 KW hepatic; antiasthma; antimicrobial; antiinflammatory; immunosuppressive;
 KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
 XX OS Homo sapiens.
 XX FT

PN WO200109328-A1.
 XX PD 08-FEB-2001.
 XX PF 03-AUG-2000; 2000WO-US21278.
 XX PR 03-AUG-1999; 99US-0146916.
 XX PR 29-FEB-2000; 2000US-0515781.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Hodge MR, Lloyd C, Welch NS;
 XX DR WPI; 2001-138653/14.
 XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
 PT -
 XX PS Disclosure; Fig 2; 145pp; English.
 XX CC The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases includes immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.
 XX SQ Sequence 440 AA;

Query Match 3.5%; Score 19; DB 22; Length 440;
 Best Local Similarity 100.0%; Pred. No. 7.8e-11;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNTHMHLFVSF 187
 |||||
 Db 167 frrlhctnrnyhmlhlfvsf 185

RESULT 13
 AAR30187
 ID AAR30187 standard; Protein; 449 AA.
 XX AC AAR30187;
 XX DT 28-APR-1993 (first entry)
 XX DE Secretin receptor.
 XX KW Rat; rat/mouse hybridoma; NG 108-15.
 XX OS Rattus rattus.
 XX FH Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /note= "signal peptide"
 FT Protein 23..449
 FT Modified-site /note= "mature secretin receptor"
 FT Modified-site 72
 FT Modified-site /note= "potential N-glycosylation site"
 FT Modified-site 100
 FT Modified-site /note= "potential N-glycosylation site"

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FT Modified-site 106 /note= "potential N-glycosylation site"
FT Modified-site 128 /note= "potential N-glycosylation site"
FT Modified-site 291 /note= "potential N-glycosylation site"
FT Domain 144..165
FT Domain 175..194
FT Domain 217..240
FT Domain 254..276
FT Domain 294..317
FT Domain 343..362
FT Domain 374..394
FT Domain
FT
FT WO9221754-A.
FT
FT 10-DEC-1992.
FT
FT 05-JUN-1992; 92WO-JP00728.
FT
FT 07-JUN-1991; 91JP-0163946.
FT
FT (OSAB-) OSAKA BIOSCIENCE INST.
FT
FT Ishihara T, Nagata S, Takahashi K;
FT
FT WPI: 1992-433652/52.
FT N-PSDB; AAQ33018.
FT
FT DNA coding for secretin receptor - is expressed in COS cells and
FT produces a receptor protein for research and clinical use
FT
FT Claim 2; Fig 1; 44pp; Japanese.
FT
FT The secretin receptor was encoded by a DNA sequence of rat origin,
FT contained in rat/mouse hybridoma NG108-15. The DNA sequence was
FT obtd. from a cDNA library derived from NG108-15 cells. Expression
FT in a suitable host allows prodn. of the receptor protein. The
FT secretin receptor protein encoded by this gene may be used in basic
FT research and in clinical tests, and is available in high yield.
FT
FT Sequence 449 AA;

Query Match 3.5%; Score 19; DB 13; Length 449;
Best Local Similarity 100.0%; Pred. No. 7.9e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNRYIHMHLFVSF 187
Db 167 frrlhctrnryihmhlfvsf 185
|||||
|||||

RESULT 14
AAAY96985
ID AAY96985 standard; Protein; 324 AA.
XX
XX AAY96985;
XX
XX 19-DEC-2000 (first entry)
DT
DE Tethered PTH-1 receptor, r-del-Nt/Ct.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; r-delta-Nt/Ct;
KW tethered receptor; osteoporosis.
```

```
XX Chimeric - Rattus sp.
OS Synthetic.
XX WO200039278-A2.
XX 06-JUL-2000.
XX 30-DEC-1999; 99WO-US31108.
XX 31-DEC-1998; 98US-0114577.
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI: 2000-452384/39.
DR N-PSDB; AAA51734.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass
XX
XX Claim 22; Fig 10; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
CC S-(L)n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tethrel activity,
CC increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrP which
CC avoids the need for regular injections to treat osteoporosis.
XX
XX Sequence 324 AA;

Query Match 3.3%; Score 18; DB 21; Length 324;
Best Local Similarity 100.0%; Pred. No. 6.2e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
Db 134 yflatnywilverglylh 151
|||||
|||||

RESULT 15
AAAY96984
ID AAY96984 standard; Protein; 335 AA.
XX
XX AAY96984;
XX
XX 31-OCT-2000 (first entry)
DT
DE Tethered PTH-1 receptor, Tether1C.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tetheric; osteoporosis.
XX
XX Chimeric - Rattus sp.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Key 1..23
FT Peptide
```

```
FT Peptide /label= PTH-1_receptor_signal_sequence
FT 24..32
FT /label= PTH_residues_1-9
FT Peptide 33..36
FT /label= linker
FT Protein 37..335
FT /label= PTH-1_receptor
FT /note= "residue 182 to 480"
XX WO200039278-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 30-DEC-1999; 99WO-US31108.
XX
XX PR 31-DEC-1998; 98US-0114577.
XX
XX PA (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX DR WPI; 2000-452384/39.
XX N-PSDB; AAA51733.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX PS Claim 22; Fig 9; 119pp; English.
XX
XX CC Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
XX S-(L)n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tetherl activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX SQ Sequence 335 AA;
XX
XX Query Match 3.3%; Score 18; DB 21; Length 335;
XX Best Local Similarity 100.0%; Pred. No. 6.4e-10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 245 YFLATNYWILVEGLYLH 262
XX |||||||||||||||
XX Db 145 yflatnywilverglylh 162
XX
XX RESULT 16
XX AAY96987
XX ID AAY96987 standard; Protein; 435 AA.
XX
XX AC AAY96987;
XX
XX DT 31-OCT-2000 (first entry)
XX
XX DE Human tethered PTH-1 receptor, hdelNT.
XX
XX KW PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tetherl; osteoporosis.
XX
```

```
OS Chimeric - Homo sapiens.
OS Synthetic.
XX
XX PN WO200039278-A2.
XX
XX PD 06-JUL-2000.
XX
XX PF 30-DEC-1999; 99WO-US31108.
XX
XX PR 31-DEC-1998; 98US-0114577.
XX
XX PA (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX DR WPI; 2000-452384/39.
XX N-PSDB; AAA51736.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX PS Example 4; Fig 18; 119pp; English.
XX
XX CC Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
XX S-(L)n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tetherl activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX SQ Sequence 435 AA;
XX
XX Query Match 3.3%; Score 18; DB 21; Length 435;
XX Best Local Similarity 100.0%; Pred. No. 8.1e-10;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 245 YFLATNYWILVEGLYLH 262
XX |||||||||||||||
XX Db 132 yflatnywilverglylh 149
XX
XX RESULT 17
XX AAB07529
XX ID AAB07529 standard; Protein; 435 AA.
XX
XX AC AAB07529;
XX
XX DT 20-OCT-2000 (first entry)
XX
XX DE A mutant parathyroid hormone (PTH) receptor designated rdelant.
XX
XX KW Mutant; parathyroid hormone; PTH; receptor; rdelant;
XX ligand binding domain.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..22
XX FT Protein 23..435
```

```
FT XX /note= "mature protein"
PN XX
XX WO200040698-A1.
PD 13-JUL-2000.
XX
PF 31-DEC-1998; 98WO-US27862.
XX
PR 31-DEC-1998; 98WO-US27862.
XX
PA (GEO ) GEN HOSPITAL CORP.
XX
PI Gardella TJ, Kronenberg HM, Potts JT;
XX
XX WPI: 2000-465971/40.
DR N-PSDB; AAA58932.
XX
XX New parathyroid hormone (PTH) receptor, r-delta-Nt, characterized by a
PT deletion of the extracellular amino-terminus ligand binding domain,
PT useful in screening assays for identifying agonists and antagonists of
PT PTH receptor activity
XX
PS Claim 17; Fig 1; 81pp; English.
XX
XX The present sequence represents a mutant parathyroid hormone (PTH)
CC receptor, designated rdelta. The polypeptide is characterised
CC by a deletion of the extracellular amino-terminus ligand binding
CC domain. The receptor has a minimal domain for ligand binding and
CC is, therefore, useful in screening assays designed for the
CC identification of agonists and antagonists of PTH receptor
CC activity.
XX
SQ Sequence 435 AA;

Query Match 3.3%; Score 18; DB 21; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.1e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYWLVEGLYLH 262
DB 134 YFLATNYWYWLVEGLYLH 151

RESULT 18
AAY96983
ID AAY96983 standard; Protein; 446 AA.
XX
XX AAY96983;
XX
XX 31-OCT-2000 (first entry)
XX
XX Tethered PTH-1 receptor, Tether1.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis.
XX
XX Chimeric - Rattus sp.
OS Synthetic.
XX
XX Location/Qualifiers
FH Key 1..23
FT Peptide /label= PTH-1_receptor_signal_sequence
FT Peptide 24..32
FT Peptide /label= PTH_residues_1-9
FT Peptide 33..36
FT Peptide /label= linker
FT Protein 37..446
FT /label= PTH-1_receptor
FT /note= "residue 182 to end"
XX
XX WO200039278-A2.
PN XX
```

```
PD 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31108.
XX
XX 31-DEC-1998; 98US-0114577.
XX
XX (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
XX WPI: 2000-452384/39.
DR N-PSDB; AAA51732.
XX
XX New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass
XX
XX Claim 22; Fig 7; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)n-B, R1-S-(L)n-R or
CC S-(L)n-R, are new. S is an amino terminal signaling functional domain
CC of parathyroid hormone (PTH); L is a linker molecule present n times
CC (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
CC binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
CC R1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
CC receptor sequence. The new compounds are used for treating mammalian
CC conditions characterized by decreases in bone mass, determining rates of
CC bone reformation, bone resorption and/or bone remodeling, treating
CC diseases and disorders associated with decreased tether1 activity,
CC increasing CAMP in a mammalian cell having PTH-1 receptors, or screening
CC for a peptide or non-peptide PTH (claimed). The new compound can be
CC administered by inhalation unlike the large native PTH or PTHrp which
CC avoids the need for regular injections to treat osteoporosis.
XX
XX Sequence 446 AA;

Query Match 3.3%; Score 18; DB 21; Length 446;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWYWLVEGLYLH 262
DB 145 YFLATNYWYWLVEGLYLH 162

RESULT 19
AAY96986
ID AAY96986 standard; Protein; 448 AA.
XX
XX AAY96986;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, Tether1.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
KW PTH-1 receptor; resorption; remodeling; tether1; osteoporosis; ss.
XX
XX Chimeric - Homo sapiens.
OS Synthetic.
XX
XX Location/Qualifiers
FH Key 1..23
FT Peptide /label= Signal_sequence
FT /note= "Human PTH-1 receptor residues 1-23"
FT Peptide 24..32
FT Peptide /label= PTH(1-9)
FT Peptide 33..36
FT /label= Linker
XX
```

```

FT Protein 37..448
FT /label= PTH-1_receptor
FT /note= "Human PTH-1 receptor residues 182-593"
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31108.
XX
XX 31-DEC-1998; 98US-0114577.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51735.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX Example 4; Fig 17; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
XX S-(L)_n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tether1 activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX Sequence 448 AA;

Query Match 3.3%; Score 18; DB 21; Length 448;
Best Local Similarity 100.0%; Pred. No. 8.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
Db 145 yflatnywilverglylh 162

RESULT 20
AAY96988
ID AAY96988 standard; Protein; 450 AA.
XX
XX AAY96988;
XX
XX 31-OCT-2000 (first entry)
XX
XX Human tethered PTH-1 receptor, Tether-R11.
XX
XX PTH; parathyroid hormone; conjugate; bone mass; bone reformation;
XX PTH-1 receptor; resorption; remodeling; tether-R11; osteoporosis; ss.
XX
XX Chimeric - Homo sapiens.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..23

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FT /label= Signal_sequence
FT /note= "Human PTH-1 receptor residues 1-23"
XX
XX Peptide 24..34
XX /label= PTH(1-11)
XX
XX Peptide 35..38
XX /label= Linker
XX
XX Protein 39..450
XX /label= PTH-1_receptor
XX /note= "Human PTH-1 receptor residues 182-593"
XX
XX WO200039278-A2.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31108.
XX
XX 31-DEC-1998; 98US-0114577.
XX
XX (GARD/) GARDELLA T J.
XX (KRON/) KRONENBERG H M.
XX (POTT/) POTTS J T.
XX (JUEP/) JUEPPNER H.
XX
XX Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX WPI; 2000-452384/39.
XX N-PSDB; AAA51737.
XX
XX New compound comprising an amino terminal signaling functional domain
XX linked to a carboxy-terminal binding portion of parathyroid hormone for
XX treating mammalian conditions characterized by decreases in bone mass
XX
XX Example 4; Fig 19; 119pp; English.
XX
XX Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or
XX S-(L)_n-R, are new. S is an amino terminal signaling functional domain
XX of parathyroid hormone (PTH); L is a linker molecule present n times
XX (where n is a positive integer 1-10 (preferably 4)); B is a C-terminal
XX binding portion of PTH(1-34) or a PTH-related protein (PTH-rp) (1-34);
XX R_1 is the PTH-1 receptor signal sequence; and R is (a portion of) PTH-1
XX receptor sequence. The new compounds are used for treating mammalian
XX conditions characterized by decreases in bone mass, determining rates of
XX bone reformation, bone resorption and/or bone remodeling, treating
XX diseases and disorders associated with decreased tether1 activity,
XX increasing cAMP in a mammalian cell having PTH-1 receptors, or screening
XX for a peptide or non-peptide PTH (claimed). The new compound can be
XX administered by inhalation unlike the large native PTH or PTHrp which
XX avoids the need for regular injections to treat osteoporosis.
XX
XX Sequence 450 AA;

Query Match 3.3%; Score 18; DB 21; Length 450;
Best Local Similarity 100.0%; Pred. No. 8.4e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
Db 147 yflatnywilverglylh 164

RESULT 21.
AAY99600
ID AAY99600 standard; Protein; 536 AA.
XX
XX AAY99600;
XX
XX 27-OCT-2000 (first entry)
XX
XX Zebrafish parathyroid hormone type-1 receptor PTH1R.
XX
XX Zebrafish; parathyroid hormone type-1 receptor; PTH1R;
XX developmental disorder; physiological disorder; neurological disorder.
KW

```

XX OS Brachydanio rerio.
 XX XX WO200032775-A1.
 XX PD 08-JUN-2000.
 XX XX 30-NOV-1999; 99WO-US28207.
 XX PF 30-NOV-1998; 98US-0110467.
 XX PR (JUEP/) JUEPPNER H.
 XX PA (RUBI/) RUBIN D A.
 XX PI Jueppner H, Rubin DA;
 XX PT WPI: 2000-412323/35.
 XX DR N-PSDB; AAA49625.
 XX XX New nucleic acids encoding parathyroid hormone receptors PTH1R and PTH3R, useful for treating diseases or disorders associated with impaired receptor functions comprises a specific nucleotide sequence -
 XX PT Claim 17; Fig 2A; 11lpp; English.
 XX CC The present sequence is the parathyroid hormone type-1 receptor (PTH1R) from the zebrafish. Its coding sequence was obtained by sequencing a cDNA clone. The gene and protein can be used to detect diseases in man where the receptor is either overexpressed or underexpressed, and they can be used to treat these diseases, which may be developmental, physiological or neurological disorders. They can also be used to identify agonists and antagonists which can be used in a similar manner. In addition, the gene can be used for chromosome identification.
 XX CC Sequence 536 AA;
 SQ Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 9.8e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNVIHMLF 184
 Db 167 gyfrlhctrnyihmlf 184
 RESULT 22
 AAY90230
 ID AAY90230 standard; Protein; 536 AA.
 XX AC AAY90230;
 XX DT 29-AUG-2000 (first entry)
 XX DE Zebrafish PTH1R receptor protein sequence.
 XX KW Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;
 KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
 XX OS Brachydanio rerio.
 XX PN WO200032771-A1.
 XX PD 08-JUN-2000.
 XX PF 28-MAY-1999; 99WO-US11883.
 XX PR 30-NOV-1998; 98US-0110467.
 XX PA (JUEP/) JUEPPNER H.
 XX PA (RUBI/) RUBIN D A.

PI Jueppner H, Rubin DA;
 XX WPI: 2000-412319/35.
 DR N-PSDB; AAA30828.
 XX PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide receptor 3 and isolated nucleic acid encoding zebrafish parathyroid hormone receptor 1 for treating disorders associated with receptor function -
 XX PT Claim 17; Fig 2a; 11lpp; English.
 XX CC This sequence is a parathyroid hormone receptor type 1 (PTH1R) receptor protein of the invention. The invention also relates to a PTH3R receptor protein. Antagonists of PTH1R or PTH3R can be used for the treatment of diseases associated with an increase in PTH1R or PTH3R activity, respectively. The peptides are used for diagnosis or prognosis of diseases and disorders associated with PTH3R or PTH1R, such as cancer. The polypeptides can be used as a molecular weight markers on sodium dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or on molecular sieve gel filtration columns. Antigenic epitope-bearing peptides and polypeptides are useful to raise antibodies, including monoclonal antibodies, that bind specifically to a polypeptide. The peptides are useful during diagnosis of diseases and disorders in mammals involving PTH1R or PTH3R receptor expression or function. Mutations that affect PTH1R or PTH3R sequence and/or expression levels of PTH1R or PTH3R could be diagnostic for patients with disease or disorders of a developmental, physiological or neurological nature. The nucleic acid molecules are valuable for chromosome identification. The mapping of DNAs to chromosomes is an important first step in correlating those sequences with genes associated with disease.
 XX CC Sequence 536 AA;
 SQ Query Match 3.3%; Score 18; DB 21; Length 536;
 Best Local Similarity 100.0%; Pred. No. 9.8e-10;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 167 GYFRLHCTRNVIHMLF 184
 Db 167 gyfrlhctrnyihmlf 184
 RESULT 23
 AAR27706
 ID AAR27706 standard; Protein; 591 AA.
 XX AC AAR27706;
 XX DT 16-MAR-1993 (first entry)
 XX DE Rat bone PTH/PTHrP receptor clone R15B prod.
 XX KW Parathyroid hormone; related protein; calcium; antagonist;
 KW antibodies; hypercalcaemia.
 XX OS Rattus rattus.
 XX PN WO9217602-A.
 XX PD 15-OCT-1992.
 XX PF 06-APR-1992; 92WO-US02821.
 XX PR 05-APR-1991; 91US-0681702.
 XX PR 06-APR-1992; 92US-0864475.
 XX PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.
 XX PI Abou-samra A, Jueppner H, Kronenberg HM, Potts JT, Schipani E;
 PI Segre GV;
 XX

DR WPI; 1992-366271/44.
 XX N-PSDB; AAR29606.
 XX
 PT New DNA encoding parathyroid hormone receptor, DNA and antibodies
 PT - for (differential) diagnosis of hypercalcaemia, and diagnosis
 PT and treatment of tumours
 XX
 PS Claim 20; Fig 3; 91pp; English.
 XX
 XX The rat bone parathyroid hormone/parathyroid hormone related
 CC protein (PTH/PTHrP) receptor protein sequence was deduced from
 CC clone R15B obtd. by screening a rat osteosarcoma (ROS) cell cDNA library
 CC to isolate those expressing functionally intact PTH/PTHrP receptor
 CC proteins, performed according to Gearing et al., (EMBO J. 8: 3676,
 CC 1989), by identifying colonies capable of binding a suitable radio-
 CC labelled ligand. The protein may be used in a therapeutic compsn. to
 CC inhibit activation of PTH or PTHrP and thus reduce the level of calcium
 CC in the blood. Cpds. capable of competing with PTH or PTHrP for binding
 CC can be identified using the protein and DNAs homologous to PTH DNA can
 CC be identified using fragments of the clone as probes. The sequence
 CC may be used for the prodn. of antibodies useful for the treatment,
 CC classification, prognosis and/or treatment of disorders related to
 CC the interaction between a cell receptor and a ligand such as in
 CC hypercalcaemia. See also AAR27704-16.
 XX
 SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 13; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 yflatnywylveglylh 307

RESULT 24
 AAR92277
 ID AAR92277 standard; Protein; 591 AA.
 AC AAR92277;
 XX
 XX 18-MAY-1996 (first entry)
 DT
 XX
 XX Rat bone PTH/PTHrP receptor.
 DE
 XX
 KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer.
 XX
 OS Rattus sp.

FH Key Location/Qualifiers
 FT Region 1..192
 FT /label= Extracellular_region
 FT 193..211
 FT /label= Transmembrane_region
 FT 212..221
 FT /label= Intracellular_region
 FT 222..240
 FT /label= Transmembrane_region
 FT 241..299
 FT /label= Extracellular_region
 FT 300..316
 FT /label= Transmembrane_region
 FT 317..325
 FT /label= Intracellular_region
 FT 326..342
 FT /label= Transmembrane_region
 FT 343..364
 FT /label= Extracellular_region
 FT 365..383

FT Region /label= Transmembrane_region
 FT 384..408
 FT /label= Intracellular_region
 FT 409..428
 FT /label= Transmembrane_region
 FT 429..444
 FT /label= Intracellular_region
 FT 445..463
 FT /label= Transmembrane_region
 FT 464..591
 FT /label= Intracellular_region
 XX
 PN US5494806-A.
 XX
 PD 27-FEB-1996.
 XX
 XX 05-APR-1991; 91US-0681702.
 PF
 XX 06-APR-1992; 92US-0864475.
 PR
 PR 05-APR-1991; 91US-0681702.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 XX
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX
 DR WPI; 1996-139028/14.
 DR N-PSDB; AAT15947.
 XX
 XX DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.
 PT
 XX
 PS Claim 1; Fig 3A-3E; 64pp; English.
 XX
 CC A rat parathyroid hormone/parathyroid hormone-related protein
 CC (PTH/PTHrP) receptor (AAR92277) is encoded by cDNA clone R15B
 CC (AAT15947) isolated from a rat osteosarcoma ROS 17/2.8 cDNA library.
 CC The receptor is a G-protein linked receptor having 7 transmembrane
 CC domains. It induces an increase in intracellular cAMP and calcium
 CC upon challenge with PTH or PTHrP. Recombinant receptor can be
 CC produced in vector/host cell systems and used in the treatment,
 CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia,
 CC to screen for (ant)agonists and to raise antibodies. Host cells
 CC expressing the receptor are used for diagnostic measurement of PTH
 CC serum levels.
 XX
 SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 17; Length 591;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYLH 262
 |||||
 Db 290 yflatnywylveglylh 307

RESULT 25
 AAR73316
 ID AAR73316 standard; Protein; 591 AA.
 XX
 AC AAR73316;
 XX
 XX 08-FEB-1999 (first entry)
 DT
 XX
 DE Parathyroid hormone receptor R15B.
 XX
 KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
 KW PTH-related hypercalcaemia; rat.
 XX
 OS Rattus sp.

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XX US5840853-A.
XX
XX PD 24-NOV-1998.
XX
XX PF 06-JUN-1995; 95US-0471494.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAV08390.
XX
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX
XX PS Claim 6; Fig 3; 63pp; English.
XX
XX CC This sequence represents the rat parathyroid hormone (PTH) receptor
XX CC R15B, which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat
XX CC opossum PTH receptor. The antibody is useful for treating disorders
XX CC characterised by overstimulation of PTH receptors by their ligand and for
XX CC the diagnosis of PTH-related hypercalcaemia.
XX
XX SQ Sequence 591 AA;

Query Match 3.3%; Score 18; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||||
Db 290 yflatnywilvegylh 307

RESULT 26
AAR92278
ID AAR92278 standard; Protein; 593 AA.
XX
XX AC AAR92278;
XX
XX DT 18-MAY-1996 (first entry)
XX
XX DE Human kidney PTH/PTHrP receptor.
XX
XX KW Parathyroid hormone; receptor; parathormone; PTH;
XX KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
XX KW hypercalcaemia; hypocalcaemia; cancer.
XX
XX OS Homo sapiens.
XX
XX PN US5494806-A.
XX
XX PD 27-FEB-1996.
XX
XX PF 05-APR-1991; 91US-0681702.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX

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DR WPI; 1996-139028/14.
DR N-PSDB; AAT15948.
XX
XX PT DNA encoding vertebrate parathyroid hormone receptor - useful for
XX PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
XX PT cancer etc.
XX
XX PS Claim 1; Fig 6A-6G; 64pp; English.
XX
XX CC A human parathyroid hormone/parathyroid hormone-related protein
XX CC (PTH/PTHrP) receptor (AAR92278) is encoded by cDNA clone HK-1
XX CC (AAT15948) isolated from a human kidney cDNA library. The receptor
XX CC induces an increase in intracellular cAMP and intracellular free
XX CC calcium when challenged by PTH or PTHrP. Recombinant receptor can
XX CC be produced in vector/host cell systems and used in the treatment,
XX CC diagnosis or prognosis of e.g. hypercalcaemia and hypocalcaemia, to
XX CC screen for (ant)agonists and to raise antibodies. Host cells
XX CC expressing the receptor can be used for diagnostic measurement of
XX CC PTH serum levels.
XX
XX SQ Sequence 593 AA;

Query Match 3.3%; Score 18; DB 17; Length 593;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
   |||||||
Db 290 yflatnywilvegylh 307

RESULT 27
AAW73317
ID AAW73317 standard; Protein; 593 AA.
XX
XX AC AAW73317;
XX
XX DT 08-FEB-1999 (first entry)
XX
XX DE Human Parathyroid hormone receptor.
XX
XX KW Parathyroid hormone receptor; PTH receptor; antibody; therapy;
XX KW PTH-related hypercalcaemia; human.
XX
XX OS Homo sapiens.
XX
XX PN US5840853-A.
XX
XX PD 24-NOV-1998.
XX
XX PF 06-JUN-1995; 95US-0471494.
XX
XX PR 06-APR-1992; 92US-0864475.
XX PR 05-APR-1991; 91US-0681702.
XX PR 06-JUN-1995; 95US-0471494.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
XX PI Schipani E, Segre GV;
XX
XX DR WPI; 1999-034124/03.
XX DR N-PSDB; AAV08391.
XX
XX PT Antibody to parathyroid hormone receptor - for diagnostic or
XX PT therapeutic use
XX
XX PS Claim 7; Fig 6; 63pp; English.
XX
XX CC This sequence represents the human parathyroid hormone (PTH) receptor
XX CC which is targeted by the antibody of the invention. The antibody
XX CC of the invention is immunoreactive with naturally occurring human, rat or

```


Db 290 yflatnnywilvegylh 307
|||||

RESULT 30

AAR27710
ID AAR27710 standard; peptide; 19 AA.

XX AC AAR27710;

XX DT 16-MAR-1993 (first entry)

XX XX

DE PTH/PTHrP receptor fragment.

XX KW Parathyroid hormone; related protein; calcium; antagonist;

XX KW antibodies; hypercalcaemia; extracellular domain.

XX XX Synthetic.

XX XX WO9217602-A.

XX PD 15-OCT-1992.

XX XX

PF 06-APR-1992; 92WO-US02821.

XX XX

PR 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

XX XX

PA (GEO) GEN HOSPITAL CORP OFFICE TECHNOLOGY.

XX XX

PI Abou-samra A, Juppner H, Kronenberg HM, Potts JT, Schipani E;

PI Segre GV;

XX XX

DR WPI; 1992-366271/44.

XX XX

XX XX

PT New DNA encoding parathyroid hormone receptor, DNA and antibodies

PT - for (differential) diagnosis of hypercalcaemia, and diagnosis

PT and treatment of tumours

XX XX

PS Claim 25; Page 5; 91pp; English.

XX XX

CC The peptide sequence shown represents an extracellular fragment of

CC parathyroid hormone/parathyroid hormone related protein

CC (PTH/PTHrP) receptor protein. The peptide is capable of binding

CC PTH or PTHrP and acting as an antagonist of these cpds. The

CC peptide may be used to inhibit activation of PTH or PTHrP and thus

CC reduce the level of calcium in the blood. Cods. capable of competing

CC with PTH or PTHrP for binding can be identified using the protein prod.

CC and DNAs homologous to PTH DNA can be identified using fragments of the

CC clone as probes. The sequence may be used for the prodn. of antibodies

CC useful for the treatment, classification, prognosis and/or treatment of

CC disorders related to the interaction between a cell receptor and a

CC ligand such as in hypercalcaemia. See also AAR27704-16.

XX XX

SQ Sequence 19 AA;

Query Match 2.6%; Score 14; DB 13; Length 19;

Best Local Similarity 100.0%; Pred. No. 6.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258

Db 6 yflatnnywilveg 19

|||||

RESULT 31

AAR92281

ID AAR92281 standard; Peptide; 19 AA.

XX AC AAR92281;

XX XX

DT 18-MAY-1996 (first entry)

XX

DE

XX

KW

KW

KW

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OS

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PN

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PD

XX

PF

XX

PR

PR

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PA

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PI

PI

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DR

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PT

PT

PT

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CC

PTH/PTHrP extracellular region fragment RP-3.

Parathyroid hormone; receptor; parathormone; PTH;

hypercalcaemia; hypocalcaemia; cancer.

Synthetic.

US5494806-A.

27-FEB-1996.

05-APR-1991; 91US-0681702.

06-APR-1992; 92US-0864475.

05-APR-1991; 91US-0681702.

(GEO) GEN HOSPITAL CORP.

Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

Schipani E, Segre GV;

WPI; 1996-139028/14.

DNA encoding vertebrate parathyroid hormone receptor - useful for

diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,

cancer etc.

Claim 21; Column 3; 64pp; English.

Parathyroid hormone (PTH) receptor fragments, including those

(AAR92279-84) based on the PTH extracellular region and those

(AAR92285-87) based on the intracellular domain, are produced by

incorporating encoding DNA sequences into a vector, and

culturing cells transformed by the vector. The peptides can be

used to raise antibodies. The peptides and antibodies are useful

in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and

hypocalcaemia, and can also be used to screen for (ant)agonists

of therapeutic appln.

Sequence 19 AA;

Query Match 2.6%; Score 14; DB 17; Length 19;

Best Local Similarity 100.0%; Pred. No. 6.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEG 258

Db 6 yflatnnywilveg 19

|||||

RESULT 32

AAW73320

ID AAW73320 standard; peptide; 19 AA.

XX AC AAW73320;

XX XX

DT 08-FEB-1999 (first entry)

DE Parathyroid hormone receptor fragment RP-3.

Parathyroid hormone receptor; PTH receptor; antibody; therapy;

PTH-related hypercalcaemia; opossum; rat; human.

Synthetic.

US5840853-A.

24-NOV-1998.

06-JUN-1995; 95US-0471494.

XX PR 06-APR-1992; 92US-0864475.
 XX PR 05-APR-1991; 91US-0681702.
 XX PR 06-JUN-1995; 95US-0471494.
 XX (GEHO) GEN HOSPITAL CORP.
 XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;
 PI Schipani E, Segre GV;
 XX WPI; 1999-034124/03.
 XX Antibody to parathyroid hormone receptor - for diagnostic or
 PT therapeutic use
 XX Claim 8; Column 19; 63pp; English.
 XX This sequence is a fragment of a opossum parathyroid hormone (PTH)
 CC receptor which is targeted by the antibody of the invention. The antibody
 CC of the invention is immunoreactive with naturally occurring human, rat or
 CC opossum PTH receptor. The antibody is useful for treating disorders
 CC characterised by overstimulation of PTH receptors by their ligand and for
 CC the diagnosis of PTH-related hypercalcaemia.
 XX SQ Sequence 19 AA;
 Query Match 2.6%; Score 14; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 245 YFLATNYWILVEG 258
 Db 6 yflatnywylveg 19
 RESULT 33
 AAB71878
 ID AAB71878 standard; Protein; 457 AA.
 XX AC AAB71878;
 XX 03-MAY-2001 (first entry)
 XX Human VIPR seven transmembrane domain.
 XX Human; h15571; immunomodulatory; vascular; hepatic; hepatic; VIPR;
 KW pituitary adenylate cyclase activating polypeptide type II receptor;
 KW antimicrobial; antiinflammatory; immunosuppressive; gene therapy;
 KW vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
 XX OS Homo sapiens.
 XX WO200109328-A1.
 XX 08-FEB-2001.
 XX 03-AUG-2000; 2000WO-US21278.
 XX 03-AUG-1999; 99US-0146916.
 XX 29-FEB-2000; 2000US-0515781.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Hodge MR, Lloyd C, Welch NS;
 XX WPI; 2001-138653/14.
 XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma

XX Disclosure; Fig 2; 145pp; English.
 XX The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases includes immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.
 XX SQ Sequence 457 AA;
 Query Match 2.4%; Score 13; DB 22; Length 457;
 Best Local Similarity 100.0%; Pred. No. 0.00011;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 172 LHCTRNYYTHMLF 184
 Db 170 lhctrnymhmlf 182
 RESULT 34
 AAR72506
 ID AAR72506 standard; Protein; 458 AA.
 XX AC AAR72506;
 XX 29-NOV-1995 (first entry)
 XX Porcine vasoactive intestinal peptide receptor protein.
 XX Porcine vasoactive intestinal peptide receptor; pig; lung tissue; probe;
 KW amplification; primer; PCR; vasodilation; gastrointestinal tract.
 XX OS Sus scrofa.
 XX EP648837-A.
 XX 19-APR-1995.
 XX 24-AUG-1994; 94EP-0306251.
 XX 25-AUG-1993; 93US-0112817.
 XX (ELIL) LILLY & CO ELI.
 XX Hsiung HM, Smith DP, Zhang X;
 XX WPI; 1995-148716/20.
 XX N-PSDB; AAQ89546.
 XX Porcine vasoactive intestinal peptide receptor and DNA - useful in
 PT receptor bio:activity assay and to screen for agents which inhibit or
 PT stimulate receptor activity
 XX Claim 3; Page 24-26; 35pp; English.
 XX The amino acid sequence of the novel porcine vasoactive intestinal
 CC peptide (pVIP) receptor. The gene was isolated from a cDNA library
 CC in the Superscript (RTM) Lambda System derived from porcine lung tissue
 CC RNA using a 700 bp probe amplified from lung tissue cDNA using primers
 CC AAQ89547-8. The gene was inserted into the plasmid pSPORT for

CC sequencing. Thereafter the gene was inserted into the plasmid pRC/CMV
CC for transfection of 293 cells and production of the recombinant protein.
CC The activity of pVIP is linked to vasodilation in the lungs and
CC gastrointestinal tract. The receptor is useful in a bioactivity assay
CC for quantifying the level of stimulation and repression of pVIP
CC enzymatic activity in response to test compounds. The receptor is also
CC useful in screening for pVIP receptor inhibitory or stimulatory agents.
XX
SQ Sequence 458 AA;

Query Match 2.4%; Score 13; DB 16; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNHYHMLF 184
Db 171 lhctnrnylhmlhf 183

RESULT 35
AAR42848
ID AAR42848 standard; Protein; 459 AA.

XX AC AAR42848;

XX DT 13-MAY-1994 (first entry)

XX DE VIP receptor protein.

XX KW vasoactive intestinal polypeptide receptor; VIP; rat; binding;
XX adenylylate cyclase activity; stimulus.

XX OS Rattus rattus.

XX PN JP05255394-A.

XX PD 05-OCT-1993.

XX PF 13-FEB-1992; 92JJP-0026607.

XX PR 13-FEB-1992; 92JJP-0026607.

XX PA (OSAB-) 2H OSAKA BIOSCIENCE KENKYUSHO.

XX DR WPI; 1993-348480/44.

XX DR N-PSDB; AAQ50349.

XX PT Vasoactive intestinal polypeptide - prep. in large amt. by
XX culturing microbe transformed by new DNA coding polypeptide

XX PS Claim 2; Page 6; 14pp; Japanese.

XX CC The sequence can be used to produce large amounts of the VIP
XX receptor peptide, by culturing a microorganism transformed by
XX the sequence.

XX SQ Sequence 459 AA;

Query Match 2.4%; Score 13; DB 14; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNHYHMLF 184
Db 171 lhctnrnylhmlhf 183

RESULT 36
AAV82704
ID AAV82704 standard; protein; 445 AA.

XX

AC AAV82704;
XX 11-AUG-2000 (first entry)
XX Human glucose-dependent insulinotropic peptide receptor protein sequence.
XX Human; glucose-dependent insulinotropic peptide receptor; GIPR;
KW GIP receptor; osteotropic hormone; bone; osteoblast; osteoporosis;
KW bone density; bone formation.
XX OS Homo sapiens.

XX PN WO2000020592-A1.

XX PD 13-APR-2000.

XX PF 07-OCT-1999; 99WO-US23365.

XX PR 07-OCT-1998; 98US-0103333.

XX PR 08-OCT-1998; 98US-0103495.

XX PA (MEDI-) MEDICAL COLLEGE GEORGIA RES INST.

XX PI Isales CM, Bollag RJ, Rasmussen H;

XX DR WPI; 2000-303777/26.

XX PT Maintaining or increasing bone density or formation for patients at
XX risk of osteoporosis comprises administering glucose-dependent
XX insulinotropic peptide -

XX PS Example 2; Fig 6; 50pp; English.

XX CC The present invention describes a method for maintaining or increasing
XX bone density or formation comprising administering to an individual a
XX glucose-dependent insulinotropic peptide (GIP) or a functionally
XX equivalent analogue. Also described are: (1) a transgenic non-human
XX mammal overexpressing GIP; and (2) a method for decreasing bone density
XX comprising administering to an individual an inhibitor of GIP binding to
XX the GIP receptor. The method is useful for maintaining or increasing
XX bone density and promoting bone formation in patients at risk of
XX osteoporosis. The present sequence represents the human GIP receptor
XX protein sequence, which is used in the exemplification of the present
XX invention.

XX SQ Sequence 445 AA;

Query Match 2.2%; Score 12; DB 21; Length 445;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRLHCTRNHYH 180

Db 141 firllhctnrnylh 152

RESULT 37
AAV51528
ID AAV51528 standard; protein; 458 AA.

XX AC AAV51528;

XX DT 15-MAY-2000 (first entry)

XX DE Human GIP receptor protein variant.

XX KW GIP receptor; glucose-dependent insulinotropic polypeptide; human;
XX pancreatic beta cell; diabetes mellitus; transgenic animal.

XX OS Homo sapiens.

XX PN EP979872-A1.

```
XX PD 16-FEB-2000.
XX PF 11-AUG-1999; 99EP-0115140.
XX PR 11-AUG-1998; 98DE-1036382.
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX PA (WOLF/) WOLF E.
XX PI Peters H, Balling R, Volz A, Goetze B, Wolf E;
XX DR WPI; 2000-162923/15.
XX PT Recombinant GIP (Glucose dependent insulinotropic polypeptide) receptor
XX PT protein used as a model for investigation of development and treatment
XX PT of diabetes mellitus -
XX PS Claim 4; Page 11-12; 24pp; German.
XX CC This invention describes a novel recombinant GIP (Glucose-dependent
XX CC insulinotropic/insulin releasing polypeptide) receptor protein (I) or
XX CC an active fragment of (I), which binds to the GIP peptide hormone without
XX CC initiating a signal transduction cascade. The invention also describes a
XX CC (1) a recombinant DNA molecule (II), encoding (I) or its active fragment,
XX CC comprising: (a) a promoter that is in the beta cells of the pancreas;
XX CC (b) a sequence that is capable of binding to the GIP peptide hormone
XX CC without initiating a signal transduction cascade; (c) a termination
XX CC sequence; and (d) a polyadenylated tail sequence, where the expression of
XX CC (II) in a suitable host causes a diabetes type phenotype. (2) a vector
XX CC containing (II) or (III); (3) a eukaryotic or prokaryotic cell line (IV),
XX CC containing (II) or (III); (4) a transgenic, non human animal (V),
XX CC containing (II); and (5) preparing (V). (V) is used as a model system for
XX CC the investigation of the development, treatment and consequences of
XX CC diabetes mellitus. Several animal models for the study of diabetes have
XX CC been developed, but the use of (I) in a transgenic animal demonstrates
XX CC the role of a defective GIP receptor in the development of diabetes,
XX CC which has not been shown before. This sequence represents the human GIP
XX CC receptor protein variant which has a deleted intracellular loop
XX CC region described in the method of the invention.
XX SQ Sequence 458 AA;

Query Match 2.2%; Score 12; DB 21; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRHLCTRNYIH 180
Db 162 frhlctrnyih 173

RESULT 38
AAY51526
ID AAY51526 standard; protein; 466 AA.
XX AC AAY51526;
XX DT 15-MAY-2000 (first entry)
XX DE Human GIP receptor protein.
XX KW GIP receptor; glucose-dependent insulinotropic polypeptide; human;
XX KW pancreatic beta.cell; diabetes mellitus; transgenic animal.
XX OS Homo sapiens.
XX PN EP979872-A1.
XX PD 16-FEB-2000.
XX PF 11-AUG-1999; 99EP-0115140.
```

```
XX PR 11-AUG-1998; 98DE-1036382.
XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.
XX PA (WOLF/) WOLF E.
XX PI Peters H, Balling R, Volz A, Goetze B, Wolf E;
XX DR WPI; 2000-162923/15.
XX PT Recombinant GIP (Glucose dependent insulinotropic polypeptide) receptor
XX PT protein used as a model for investigation of development and treatment
XX PT of diabetes mellitus -
XX PS Disclosure; Page 9-10; 24pp; German.
XX CC This invention describes a novel recombinant GIP (Glucose-dependent
XX CC insulinotropic/insulin releasing polypeptide) receptor protein (I) or
XX CC an active fragment of (I), which binds to the GIP peptide hormone without
XX CC initiating a signal transduction cascade. The invention also describes a
XX CC (1) a recombinant DNA molecule (II), encoding (I) or its active fragment,
XX CC comprising: (a) a promoter that is in the beta cells of the pancreas;
XX CC (b) a sequence that is capable of binding to the GIP peptide hormone
XX CC without initiating a signal transduction cascade; (c) a termination
XX CC sequence; and (d) a polyadenylated tail sequence, where the expression of
XX CC (II) in a suitable host causes a diabetes type phenotype. (2) a vector
XX CC containing (II); (3) a eukaryotic or prokaryotic cell line (IV),
XX CC containing (II) or (III); (4) a transgenic, non human animal (V),
XX CC containing (II); and (5) preparing (V). (V) is used as a model system for
XX CC the investigation of the development, treatment and consequences of
XX CC diabetes mellitus. Several animal models for the study of diabetes have
XX CC been developed, but the use of (I) in a transgenic animal demonstrates
XX CC the role of a defective GIP receptor in the development of diabetes,
XX CC which has not been shown before. This sequence represents the human GIP
XX CC receptor protein described in the method of the invention.
XX SQ Sequence 466 AA;

Query Match 2.2%; Score 12; DB 21; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRRHLCTRNYIH 180
Db 162 frhlctrnyih 173

RESULT 39
AAB71870
ID AAB71870 standard; Protein; 466 AA.
XX AC AAB71870;
XX DT 03-MAY-2001 (first entry)
XX DE Human GIPR seven transmembrane domain.
XX KW Human; GIPR; glucose-dependent insulinotropic polypeptide receptor;
XX KW h15571; immunomodulatory; vascular; hepatic; antiasthma; antimicrobial;
XX KW antiinflammatory; immunosuppressive; gene therapy; vaccine;
XX KW G-protein coupled receptor; GPCR; liver fibrosis;
XX KW respiratory disorder; infection; chronic inflammatory disease;
XX KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
XX OS Homo sapiens.
XX PN WO200109328-A1.
XX PD 08-FEB-2001.
XX PF 03-AUG-2000; 2000WO-US21278.
```

PR 03-AUG-1999; 99US-0145916.
PR 29-FEB-2000; 2000US-0515781.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Hodge MR, Lloyd C, Welch NS;
XX
DR WPI; 2001-138653/14.
XX
XX Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
PT
XX
XX
PS Disclosure: Fig 2; 145pp; English.
XX
XX The present sequence is a human G-protein coupled receptor (GPCR) used
CC for comparison with the seven transmembrane domain of a novel GPCR
CC designated h1571. h1571 GPCR polynucleotides and polypeptides may be
CC used in the prevention, treatment and diagnosis of diseases associated
CC with inappropriate GPCR expression. Such diseases includes immune,
CC haematological, fibrotic, hepatic and respiratory disorders including
CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
CC graft rejection, graft versus host disease, cystic fibrosis and, in
CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
CC in the production of antibodies against GPCR and in assays to identify
CC modulators (agonists and antagonists) of GPCR expression and activity.
CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
CC used as diagnostic agents for detecting the presence of GPCR
CC polypeptides in samples.
XX
XX
SQ Sequence 466 AA;

Query Match 2.2%; Score 12; DB 22; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIH 180
DB 162 frrlhctrnviyh 173
|||||

RESULT 40
AAR70138
ID AAR70138 standard; Peptide; 11 AA.
XX
AC AAR70138;
XX
DT 09-OCT-1995 (first entry)
XX
DE Opossum parathyroid hormone transmembrane domain.
XX
KW Secretin family; G-protein linked receptor; transmembrane domain.
XX
OS Opossum.
XX
PN W09506724-A.
XX
PD 09-MAR-1995.
XX
PF 01-SEP-1994; 94WO-GB01892.
XX
PR 01-SEP-1993; 93GB-0018105.
XX
PA (WEDI-) MEDICAL RES COUNCIL.
XX
PI Harmar AJ, Lutz EM, West KM;
XX
DR WPI; 1995-115440/15.
DR N-PSDB; AAQ83212.
XX

PT New nucleic acid encoding vasoactive intestinal peptide receptor
PT - and related polypeptides, vectors, transformed cells, probes
PT and antibodies, useful for diagnosis and for screening potential
XX agonists and antagonists.
PS Disclosure: Figure 3; 39pp; English.
XX
XX VIP2 is an adenylate cyclase-linked VIP receptor from rat brain. The
CC VIP2 receptor was identified by PCR of rat pituitary cDNA using
CC degenerate oligo primers corresp. to the third and seventh
CC transmembrane domains of the secretin family of G-protein linked
CC receptors (Q83212 and Q83213 respectively). The primers were based
CC on the third and seventh transmembrane domains of the rat secretin,
CC pig calcitonin and opossum parathyroid hormone (PTH) receptors (see
CC R70137-R701410. Full length cDNAs were isolated from an olfactory
CC bulb cDNA library. The sequence has been submitted to the EMBL/GenBank
CC database under accession No. Z25885 (see Q83211/R70136). A
CC polynucleotide probe comprising a labelled DNA or RNA sequence
CC capable of specifically binding to a gene for VIP2 receptor is
CC claimed.
XX
SQ Sequence 11 AA;

Query Match 2.0%; Score 11; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 NYWVILVEGLY 260
DB 1 nyywvllvegly 11
|||||

RESULT 41
AAY90231
ID AAY90231 standard; Protein; 523 AA.
XX
AC AAY90231;
XX
DT 29-AUG-2000 (first entry)
XX
DE Zebrafish PTH3R receptor protein sequence.
XX
KW Zebrafish; PTH1R receptor; PTH3R receptor; diagnosis; cancer;
KW parathyroid hormone type 1 receptor; parathyroid hormone type 3 receptor.
OS Brachydanio rerio.
XX
PN W0200032771-A1.
XX
PD 08-JUN-2000.
XX
PF 28-MAY-1999; 99WO-US11883.
XX
PR 30-NOV-1998; 98US-0110467.
XX
PA (JUEP/) JUEPPNER H.
PA (RUBI/) RUBIN D A.
XX
PI Jueppner H, Rubin DA;
XX
DR WPI; 2000-412319/35.
DR N-PSDB; AAA30829.
XX
PT Novel zebrafish parathyroid hormone/parathyroid hormone related peptide
PT receptor 3 and isolated nucleic acid encoding zebrafish parathyroid
PT hormone receptor 1 for treating disorders associated with receptor
XX function -
PS Claim 38; Fig 2b; 111pp; English.
XX
XX This sequence is a parathyroid hormone receptor type 3 (PTH3R)
CC receptor protein of the invention. The invention also relates to a PTH1R

CC receptor protein. Antagonists of PTHrP or PTH3R can be used for the
 CC treatment of diseases associated with an increase in PTHrP or PTH3R
 CC activity, respectively. The peptides are used for diagnosis or prognosis
 CC of diseases and disorders associated with PTH3R or PTHrP, such as cancer.
 CC The polypeptides can be used as a molecular weight markers on sodium
 CC dodecyl sulphate polyacrylamide gel electrophoresis (SDS-PAGE) gels, or
 CC on molecular sieve gel filtration columns. Antigenic epitope-bearing
 CC peptides and polypeptides are useful to raise antibodies, including
 CC monoclonal antibodies, that bind specifically to a polypeptide. The
 CC peptides are useful during diagnosis of diseases and disorders in
 CC mammals involving PTHrP or PTH3R receptor expression or function.
 CC Mutations that affect PTHrP or PTH3R sequence and/or expression levels
 CC of PTHrP or PTH3R could be diagnostic for patients with disease or
 CC disorders of a developmental, physiological or neurological nature. The
 CC nucleic acid molecules are valuable for chromosome identification. The
 CC mapping of DNAs to chromosomes is an important first step in
 CC correlating those sequences with genes associated with disease.
 XX
 SQ Sequence 523 AA;

Query Match 2.0%; Score 11; DB 21; Length 523;
 Best Local Similarity 100.0%; Pred. No. 0.014; Mismatches 0; Indels 0; Gaps 0;
 Matches 11; Conservative 0;

QY 252 YWILVEGLYLH 262
 |||||
 DB 236 ywilverglylh 246

RESULT 42

AAY99601
 ID AAY99601 standard; Protein; 542 AA.

AC AAY99601;

XX 27-OCT-2000 (first entry)

DE Zebrafish parathyroid hormone type-3 receptor PTH3R.

KW Zebrafish; parathyroid hormone type-3 receptor; PTH3R;
 KW developmental disorder; physiological disorder; neurological disorder.

OS Brachydanio rerio.

PN W0200032775-Al.

XX 08-JUN-2000.

PF 30-NOV-1999; 99WO-US28207.

PR 30-NOV-1998; 98US-0110467.

PA (JUEP/) JUEPPNER H.

PA (RUBI/) RUBIN D A.

PI Jueppner H, Rubin DA;

DR WPI; 2000-412323/35.

XX N-PSDB; AAA48446.

PT New nucleic acids encoding parathyroid hormone receptors PTHrP and
 PT PTH3R, useful for treating diseases or disorders associated with
 PT impaired receptor functions comprises a specific nucleotide sequence -

PS Claim 23; Fig 2B; 11lpp; English.

XX The present sequence is the parathyroid hormone type-3 receptor
 CC (PTH3R) from the zebrafish. Its coding sequence was obtained by
 CC sequencing a cDNA clone. The gene and protein can be used to detect
 CC diseases in man where the receptor is either overexpressed or
 CC underexpressed, and they can be used to treat these diseases, which may
 CC be developmental, physiological or neurological disorders. They can also

CC be used to identify agonists and antagonists which can be used in a
 CC similar manner. In addition, the gene can be used for chromosome
 CC identification.

SQ Sequence 542 AA;

Query Match 2.0%; Score 11; DB 21; Length 542;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262

|||||

DB 236 ywilverglylh 246

RESULT 43

AAR92285
 ID AAR92285 standard; Peptide; 10 AA.

XX AAR92285;

XX 18-MAY-1996 (first entry)

DE PTH/PTHrP intracellular region fragment RPI-7.

KW Parathyroid hormone; receptor; parathormone; PTH;
 KW parathyroid hormone-related protein; PTHrP; calcium; homeostasis;
 KW hypercalcaemia; hypocalcaemia; cancer.

OS Synthetic.

PN US5494806-A.

XX 27-FEB-1996.

PF 05-APR-1991; 91US-0681702.

PR 06-APR-1992; 92US-0864475.

XX 05-APR-1991; 91US-0681702.

PA (GEO) GEN HOSPITAL CORP.

XX Abou-Samra A, Juppner H, Kronenberg HM, Potts JT;

PI Schipani E, Segre GV;

XX WPI; 1996-139028/14.

PT DNA encoding vertebrate parathyroid hormone receptor - useful for
 PT diagnosis and treatment of e.g. hypercalcaemia, hypo-calcaemia,
 PT cancer etc.

XX Disclosure; Column 3; 64pp; English.

XX Parathyroid hormone (PTH) receptor fragments, including those
 CC (AAR92279-84) based on the PTH extracellular region and those
 CC (AAR92285-87) based on the intracellular domain, are produced by
 CC incorporating encoding DNA sequences into a vector, and
 CC culturing cells transformed by the vector. The peptides can be
 CC used to raise antibodies. The peptides and antibodies are useful
 CC in the treatment, diagnosis or prognosis of e.g. hypercalcaemia and
 CC hypocalcaemia, and can also be used to screen for (ant)agonists
 CC of therapeutic appln.

SQ Sequence 10 AA;

Query Match 1.8%; Score 10; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRYN 178
 |||||

```
Db      1 frrlhctry 10

RESULT 44
AAR57829
ID AAR57829 standard; Protein; 162 AA.
XX
XX AAR57829;
AC
XX 03-OCT-1994 (first entry)
DT
XX Human GR C-terminal (clone 40-2-2).
DE
XX Rat; human; glucagon receptor; transgenic animal; metabolism; model;
KW amplification; primer; polymerase chain reaction; PCR.
XX
XX Homo sapiens.
OS
XX WO9405789-A.
PN
XX 17-MAR-1994.
PD
XX 30-AUG-1993; 93WO-US08174.
PF
XX 28-AUG-1992; 92US-0938331.
PR 01-JUL-1993; 93US-0086631.
XX
XX (ZYMO ) ZYMOGENETICS INC.
PA
XX Foster DC, Grant FJ, Jelinek LJ, Kindsvogle WR;
PI Kuijper JL, Lok S, O'Hara PJ, Sheppard PO;
XX
XX WPI; 1994-101194/12.
DR N-PSDB; AAO67247.
XX
XX New recombinant glucagon receptors and antibodies - useful to
PT produce model transgenic animals for study and with therapeutic
PT applications
XX
XX Example 5; Page 86-87; 112pp; English.
PS
XX
XX Example 5 describes the isolation of human GR.
CC The GR coding sequence was constructed from partial clone
CC p9A11 (5' end) and clone 40-2-2 (3' end).
CC Host cells contg. GR DNA may be used for the prodn. of
CC recombinant GR. GR DNA may also be expressed in non-human
CC transgenic animals, pref. mice. Such animals may be readily
CC used as models to study the role of the glucagon receptor
CC in metabolism.
XX
XX Sequence 162 AA;

Query Match 1.8%; Score 10; DB 15; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
DB 99 lveglylhl 108
|||||

RESULT 45
AAW68067
ID AAW68067 standard; Protein; 222 AA.
XX
XX AAW68067;
AC
XX 23-SEP-1998 (first entry)
DT
XX Human glucagon-like peptide-2 (GLP-2) receptor fragment.
DE
XX Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;
KW
```

```
receptor ligand screening.
KW
XX Homo sapiens.
OS
XX WO9825955-A2.
PN
XX 18-JUN-1998.
PD
XX 15-DEC-1997; 97WO-CA00969.
PF
XX 24-APR-1997; 97US-0845546.
PR 13-DEC-1996; 96US-0767224.
PR 24-JAN-1997; 97US-0787721.
XX
XX (ALIX ) ALLELIX BIOPHARMACEUTICALS INC.
PA
XX Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;
XX WPI; 1998-348449/30.
DR N-PSDB; AAV39157.
XX
XX New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.
PT isolating homologues and GLP-2 receptor ligand screening
PT
XX Disclosure; Fig 5; 54pp; English.
PS
XX This is a human glucagon-like peptide-2 (GLP-2) receptor fragment. The
CC specification provides the sequences of human and rat GLP-2 receptors.
CC Genetically engineered host cells containing the GLP-2 receptor encoding
CC nucleic acid sequences operably linked to expression elements can be
CC used to produce the recombinant proteins. These cells can be used in a
CC method for identifying GLP-2 receptor ligands which comprises incubating
CC a candidate ligand with the cell, and determining whether binding has
CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding
CC homologues. They can also be used for constructing cell lines for GLP-2
CC receptor ligand screening.
XX
XX Sequence 222 AA;

Query Match 1.8%; Score 10; DB 19; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYIHM 181
DB 20 lhctrylhm 29
|||||

RESULT 46
AAR50047
ID AAR50047 standard; Protein; 477 AA.
XX
XX AAR50047;
AC
XX 03-OCT-1994 (first entry)
DT
XX Human glucagon receptor.
DE
XX Rat; human; glucagon receptor; transgenic animal; metabolism; model;
KW signal sequence; transmembrane domain; glycosylation site.
XX
XX Homo sapiens.
OS
XX WO9405789-A.
PN
XX 17-MAR-1994.
PD
XX 30-AUG-1993; 93WO-US08174.
PF
XX 28-AUG-1992; 92US-0938331.
PR 01-JUL-1993; 93US-0086631.
XX
```

XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Foster DC, Grant FU, Jelinek LJ, Kindsvogle WR;
 XX PI Kuijper JL, Lok S, O'Hara PJ, Sheppard PO;
 XX DR WPI; 1994-101194/12.
 XX DR N-PSDB; AAQ58776.
 XX PT New recombinant glucagon receptors and antibodies - useful to
 PT produce model transgenic animals for study and with therapeutic
 PT applications
 XX PS Claim 4; Page 91-95; 112pp; English.
 XX CC Rat and human glucagon receptor (GR) DNA was isolated.
 CC Host cells contg. GR DNA may be used for the prodn. of
 CC recombinant GR. GR DNA may also be expressed in non-human
 CC transgenic animals, pref. mice. Such animals may be readily
 CC used as models to study the role of the glucagon receptor
 CC in metabolism.
 XX SQ Sequence 477 AA;

Query Match 1.8%; Score 10; DB 15; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264
 Db 243 lveglylhnl 252
 |||||||||

RESULT 47

AA071872
 ID AAB71872 standard; Protein; 477 AA.
 XX AC AAB71872;
 XX DT 03-MAY-2001 (first entry)
 XX DE Human GLR seven transmembrane domain.
 XX KW Human; GLR; glucagon receptor; h15571; immunomodulatory; vascular;
 KW hepatic; antilasthma; antimicrobial; antiinflammatory; immunosuppressive;
 KW gene therapy; vaccine; G-protein coupled receptor; GPCR; liver fibrosis;
 KW respiratory disorder; infection; chronic inflammatory disease;
 KW organ-specific autoimmunity; graft rejection; cystic fibrosis.
 XX OS Homo sapiens.
 XX PN WO200109328-A1.
 XX PD 08-FEB-2001.
 XX PF 03-AUG-2000; 2000WO-US21278.
 XX PR 03-AUG-1999; 99US-0146916.
 XX PR 29-FEB-2000; 2000US-0515781.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Hodge MR, Lloyd C, Weich NS;
 XX DR WPI; 2001-138653/14.
 XX PT Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful
 PT for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
 XX PS Disclosure; Fig 2; 145pp; English.

CC The present sequence is a human G-protein coupled receptor (GPCR) used
 CC for comparison with the seven transmembrane domain of a novel GPCR
 CC designated h15571. h15571 GPCR polynucleotides and polypeptides may be
 CC used in the prevention, treatment and diagnosis of diseases associated
 CC with inappropriate GPCR expression. Such diseases includes immune,
 CC haematological, fibrotic, hepatic and respiratory disorders including
 CC asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic
 CC infections, chronic inflammatory diseases, organ-specific autoimmunity,
 CC graft rejection, graft versus host disease, cystic fibrosis and, in
 CC particular, liver fibrosis. The GPCR polypeptides may be used as antigens
 CC in the production of antibodies against GPCR and in assays to identify
 CC modulators (agonists and antagonists) of GPCR expression and activity.
 CC The anti-GPCR antibodies and GPCR antagonists may also be used to down
 CC regulate GPCR expression and activity. The anti-GPCR antibodies may be
 CC used as diagnostic agents for detecting the presence of GPCR
 CC polypeptides in samples.
 XX SQ Sequence 477 AA;

Query Match 1.8%; Score 10; DB 22; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264
 Db 243 lveglylhnl 252
 |||||||||

RESULT 48

AAW68066
 ID AAW68066 standard; Protein; 550 AA.
 XX AC AAW68066;
 XX DT 23-SEP-1998 (first entry)
 XX DE Rat glucagon-like peptide-2 (GLP-2) receptor.
 KW Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;
 KW receptor ligand screening.
 XX OS Rattus sp.
 XX FH Key Location/Qualifiers
 FT Peptide 1..66
 FT Protein /note= "signal sequence"
 FT 67..550
 FT /note= "mature protein"
 XX PN WO9825955-A2.
 XX PD 18-JUN-1998.
 XX PF 15-DEC-1997; 97WO-CA00969.
 XX PR 24-APR-1997; 97US-0845546.
 XX PR 13-DEC-1996; 96US-0767224.
 XX PR 24-JAN-1997; 97US-0787721.
 XX PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 XX PI Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;
 XX DR WPI; 1998-348449/30.
 XX DR N-PSDB; AAV39156.
 XX PT New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.
 PT isolating homologues and GLP-2 receptor ligand screening
 XX PS Claim 16; Fig 2; 54pp; English.
 XX CC This represents a rat glucagon-like peptide-2 (GLP-2) receptor. The

CC specification provides the sequences of human and rat GLP-2 receptors.
CC Genetically engineered host cells containing the GLP-2 receptor encoding
CC nucleic acid sequences operably linked to expression elements can be
CC used to produce the recombinant proteins. These cells can be used in a
CC method for identifying GLP-2 receptor ligands which comprises incubating
CC a candidate ligand with the cell, and determining whether binding has
CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding
CC homologues. They can also be used for constructing cell lines for GLP-2
CC receptor ligand screening.
XX
SQ Sequence 550 AA;

Query Match 1.8%; Score 10; DB 19; Length 550;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHM 181
Db 206 lhctrnyihm 215
|||||

RESULT 49
AAW68065
ID AAW68065 standard; Protein; 553 AA.
XX
AC AAW68065;
XX
DT 23-SEP-1998 (first entry)
XX
DE Human glucagon-like peptide-2 (GLP-2) receptor.
XX
KW Glucagon-like peptide-2 receptor; GLP-2 receptor; human; rat;
KW receptor ligand screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..66
FT /note= "signal sequence"
FT Protein 67..553
FT /note= "mature protein"
XX
PN WO9825955-A2.
XX
PD 18-JUN-1998.
XX
PF 15-DEC-1997; 97WO-CA00969.
XX
PR 24-APR-1997; 97US-0845546.
PR 13-DEC-1996; 96US-0767224.
PR 24-JAN-1997; 97US-0787721.
XX
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
XX
PI Fan E, Gupta AK, McCallum K, Munroe DG, Vyas TB;
XX
DR WPI; 1998-348449/30.
DR N-PSDB; AAV39155.
XX
PT New, e.g. rat glucagon-like peptide-2 receptor - useful for, e.g.
PT Isolating homologues and GLP-2 receptor ligand screening
XX
PS Claim 17; Fig 6A-B; 54pp; English.
XX

CC This represents a human glucagon-like peptide-2 (GLP-2) receptor. The
CC specification provides the sequences of human and rat GLP-2 receptors.
CC Genetically engineered host cells containing the GLP-2 receptor encoding
CC nucleic acid sequences operably linked to expression elements can be
CC used to produce the recombinant proteins. These cells can be used in a
CC method for identifying GLP-2 receptor ligands which comprises incubating
CC a candidate ligand with the cell, and determining whether binding has

CC occurred between the GLP-2 receptor and the candidate ligand. The GLP-2
CC receptor polynucleotides can be used to isolate GLP-2 receptor-encoding
CC homologues. They can also be used for constructing cell lines for GLP-2
CC receptor ligand screening.
XX
SQ Sequence 553 AA;

Query Match 1.8%; Score 10; DB 19; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHM 181
Db 206 lhctrnyihm 215
|||||

Search completed: September 21, 2001, 17:09:55
Job time: 203 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:08:32 ; Search time 19.6 Seconds
(without alignments)
2102.573 Million cell updates/sec

Title: US-09-236-468a-2
Perfect score: 541
Sequence: 1 MAWLGAHLVWGLMLGSL.....DDILMEKSPRMESNPDTBG 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues
Word size: 10

Total number of hits satisfying chosen parameters: 17

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR_68.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	363	67.1	550	A57519	parathyroid hormon
2	25	4.6	585	A39286	parathyroid hormon
3	19	3.5	440	JC2532	secretin receptor
4	19	3.5	449	S16319	secretin receptor
5	18	3.3	589	I59297	parathyroid' hormon
6	18	3.3	591	S44203	parathyroid' hormon
7	18	3.3	591	I54195	parathyroid' hormon
8	18	3.3	593	A49191	parathyroid' hormon
9	13	2.4	455	I53273	gastric inhibitory
10	13	2.4	459	JH0594	vasoactive intesti
11	13	2.4	460	JC2194	vasoactive intesti
12	13	2.4	462	JC2462	gastric inhibitory
13	13	2.4	495	JC2195	vasoactive intesti
14	12	2.2	466	G02234	gastric inhibitory
15	12	2.2	466	S66676	glucose-dependent
16	12	2.2	491	I37411	glucose-dependent
17	10	1.8	477	JC2041	glucagon receptor

ALIGNMENTS

RESULT 1
A57519
parathyroid hormone receptor 2 precursor - human
N:Alternate names: PTH2 receptor
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 24-Nov-1999
C:Accession: A57519

R:Usdin, T.B.; Gruber, C.; Bonner, T.
J. Biol. Chem. 270, 15455-15458, 1995
A:Title: Identification and functional expression of a receptor selectively recognizing
A:Reference number: A57519; MUID:95318121
A:Accession: A57519
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-550 <USD>
A:Cross-references: GB:U25128; NID:g887966; PIDN:AAC50157.1; PID:g887967
C:Genetics:
A:Gene: GDB:PTH2; PTHR2
A:Cross-references: GDB:731977; OMIM:601469
A:Map position: 2q33-2q35
C:Superfamily: glucagon receptor
C:Keywords: hormone receptor

Query Match 67.1%; Score 363; DB 2; Length 550;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4 LGASLHVWGLMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAQLOEGCNC 63
Db 4 LGASLHVWGLMLGSCLLARAQLDSGTITIEEQIVLVKAKVQCELNITAQLOEGCNC 63
Qy 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWANY 123
Db 64 FPEWDGLICWPRGTGKISAVPCPPYIYDFNKHGVAFRHCNPNGTWDFMHSLNKTWANY 123
Qy 124 DCLRFLQPDISIGKQEFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183
Db 124 DCLRFLQPDISIGKQEFCEERLYVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNHYHML 183
Qy 184 FVSMPLRATSFVKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYIGCKTAVVMF 243
Db 184 FVSMPLRATSFVKDRVVAHIGVKELESIMODDPQNSIEATSDVKSOYIGCKTAVVMF 243
Qy 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFILIGWGFPAFVAANAVARATLAD 303
Db 244 IYFLATNYWILVEGLYLHNLIFVAFSDTKYLMGFILIGWGFPAFVAANAVARATLAD 303
Qy 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRLVATKIWETNAVGHDFRKYRKLAK 363
Db 304 ARCWELSGADIKWIYQAPILAAIGLNFILNTVRLVATKIWETNAVGHDFRKYRKLAK 363
Qy 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFGQFVSIYCYCNGEVOAE 423
Db 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWEIRMHCELFNSFGQFVSIYCYCNGEVOAE 423
Qy 424 VKMWSRNLSVDNKRTPPCGSRRCGSLVTTVTHSTSSQSOVAA 467
Db 424 VKMWSRNLSVDNKRTPPCGSRRCGSLVTTVTHSTSSQSOVAA 467

RESULT 2
A39286
parathyroid hormone / parathyroid hormone-related peptide - North American opossum
C:Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opo
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 11-Jan-2000
C:Accession: A39286
R:Jueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.F.; Schipani, E.; Richards, J.
Science 254, 1024-1026, 1991
A:Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-
A:Reference number: A39286; MUID:92054592
A:Accession: A39286
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-585 <JUE>
A:Cross-references: GB:M74445
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

```
Query Match          4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 5e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRLHCTRNTHMHLFVSEMLRA 191
      |||
Db 207 GYFRLHCTRNTHMHLFVSEMLRA 231

RESULT 3
JC2532
secretin receptor - human
C:Species: Homo sapiens (man)
C>Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 05-Nov-1999
C:Accession: JC2532
R:Jiang, S.; Ulrich, C.
Biochem. Biophys. Res. Commun. 207, 883-890, 1995
A:Title: Molecular cloning and functional expression of a human pancreatic secretin receptor
A:Reference number: JC2532; MUID:95169147
A:Accession: JC2532
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-440 <JIA>
A:Cross-references: EMBL:U20178; NID:g662795; PIDN:AAC50106.1; PID:g662796
A:Experimental source: pancreas
C:Genetics:
A:Gene: GDB:SCTR
A:Cross-references: GDB:270546; OMIM:182098
A:Map position: 2q14.1-2q14.1
C:Superfamily: glucagon receptor

Query Match          3.5%; Score 19; DB 2; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.4e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNTHMHLFVSF 187
      |||
Db 167 FRRLHCTRNTHMHLFVSF 185

RESULT 4
S16319
secretin receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S16319
R:Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO J. 10, 1635-1641, 1991
A:Title: Molecular cloning and expression of a cDNA encoding the secretin receptor.
A:Reference number: S16319; MUID:91266890
A:Accession: S16319
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-449 <ISH>
A:Cross-references: EMBL:X59132; NID:g57228; PIDN:CAA41849.1; PID:g57229
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match          3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNTHMHLFVSF 187
      |||
Db 167 FRRLHCTRNTHMHLFVSF 185

RESULT 5
I59297
parathyroid hormone/parathyroid hormone related-peptide receptor - mouse
C:Species: Mus musculus (house mouse)
```

```
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I59297
R:McCuag, K.A.; Clarke, J.C.; White, J.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 5051-5055, 1994
A:Title: Molecular cloning of the gene encoding the mouse parathyroid hormone/parathyroid hormone-related peptide receptor
A:Reference number: I59297; MUID:94255468
C:Accession: I59297
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-589 <RES>
A:Cross-references: GB:L34611; NID:g530149; PIDN:AAA40011.1; PID:g530151
C:Genetics:
A:Gene: PTHR
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2;
C:Superfamily: glucagon receptor

Query Match          3.3%; Score 18; DB 2; Length 589;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
      |||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 6
S44203
parathyroid hormone-related peptide receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jan-2000
C:Accession: S44203
R:Karperlen, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boon
submitted to the EMBL Data Library, April 1994
A:Description: Expression pattern of parathyroid hormone/parathyroid hormone related
A:Reference number: S44203
A:Accession: S44203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-591 <KAR>
A:Cross-references: EMBL:X78936; NID:g474828; PIDN:CAA55536.1; PID:g474829
C:Superfamily: glucagon receptor

Query Match          3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
      |||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 7
I54195
parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 11-Jan-2000
C:Accession: I54195; A42698
R:Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Riv
Genomics 20, 20-26, 1994
A:Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide recepto
and rat genomes.
A:Reference number: I54195; MUID:94292182
A:Accession: I54195
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-591 <RES>
A:Cross-references: GB:L19475; NID:g467316; PIDN:AAA68098.1; PID:g467317
R:Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.;
Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A:Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid
n of both cAMP and inositol trisphosphates and increases intracellular free calcium.
```


A:Reference number: A42698; MUID:92212903
A:Accession: A42698
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-585, 'G', 587-591 <ABO>
A:Experimental source: ROS 17/2.8 osteosarcoma cells
A:Note: sequence extracted from NCBI backbone (NCBIP:92187)
C:Superfamily: glucagon receptor

Query Match 3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 8

A49191
parathyroid hormone/PTH-related peptide receptor - human
N:Alternate names: parathyroid hormone/parathyroid hormone related peptide receptor
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 11-Jan-2000
C:Accession: I38139; A49191; I38113; G01562; S29610
R:Schipani, E.; Weinstein, L.S.; Bergwitz, C.; Iida-Klein, A.; Kong, X.F.; Stuhmann, M.
Kronenberg, H.M.; Abou-Samra, A.B.; Segre, G.V.; Jueppner, H.
J. Clin. Endocrinol. Metab. 80, 1611-1621, 1995
A:Title: Pseudohypoparathyroidism type 1b is not caused by mutations in the coding exons
A:Reference number: I38139; MUID:95263723
A:Accession: I38139
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-593 <RES>
A:Cross-references: EMBL:U022409; NID:g8977594; PIDN:AAB60657.1; PID:g8977596
R:Schipani, E.; Karga, H.; Karapilis, A.C.; Potts Jr., J.T.; Kronenberg, H.M.; Segre, G.V.
Endocrinology 132, 2157-2165, 1993
A:Title: Identical complementary deoxyribonucleic acids encode a human renal and bone pa
A:Reference number: A49191; MUID:93238641
A:Accession: A49191
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-593 <SCH>
A:Cross-references: GB:L04308; NID:g190721; PIDN:AAA36525.1; PID:g190722
A:Note: sequence extracted from NCBI backbone (NCBIN:130233, NCBIP:130234)
R:Schneider, H.; Feyen, J.H.; Seuwen, K.; Movva, N.R.
Eur. J. Pharmacol. 246, 149-155, 1993
A:Title: Cloning and functional expression of a human parathyroid hormone receptor.
A:Reference number: I38113; MUID:93387403
A:Accession: I38113
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-593 <RE2>
A:Cross-references: EMBL:X68596; NID:g396812; PIDN:CAA48589.1; PID:g396813
R:Levine, M.
submitted to the EMBL Data Library, November 1994
A:Reference number: G07787
A:Accession: G01562
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-593 <LEV>
A:Cross-references: EMBL:U17418; NID:g596129; PIDN:AAA56774.1; PID:g596130
C:Genetics:
A:Introns: 25/3; 60/1; 105/1; 142/1; 181/3; 213/2; 278/3; 330/1; 350/2; 372/3; 404/2; 45
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 3.3%; Score 18; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 7.3e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYWILVEGLYLH 262
|||||
Db 290 YFLATNYWILVEGLYLH 307

RESULT 9

I53273
gastric inhibitory polypeptide receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 24-Sep-1999
C:Accession: I53273
R:Uddin, T.B.; Mezey, E.; Button, D.C.; Brownstein, M.J.; Bonner, T.I.
Endocrinology 133, 2861-2870, 1993
A:Title: Gastric inhibitory polypeptide receptor, a member of the secretin-vasoactive
A:Reference number: I53273; MUID:94062667
A:Accession: I53273
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-455 <RES>
A:Cross-references: GB:L19660; NID:g431448; PIDN:AAC37637.1; PID:g431449
C:Superfamily: glucagon receptor

Query Match 2.4%; Score 13; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNRYIHM 181
|||||
Db 159 FRLHCTRNRYIHM 171

RESULT 10

JH0594
vasoactive intestinal peptide receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: JH0594; S56014
R:Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
Neuron 8, 811-819, 1992
A:Title: Functional expression and tissue distribution of a novel receptor for vasoac
A:Reference number: JH0594; MUID:92232309
A:Accession: JH0594
A:Molecule type: mRNA
A:Residues: 1-459 <ISH>
A:Cross-references: GB:M86835; NID:g207640; PIDN:AAA42331.1; PID:g207641
R:Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A:Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene
A:Reference number: S56014; MUID:97104266
A:Accession: S56014
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-26 <PEI>
A:Cross-references: EMBL:U10635; NID:g505752; PIDN:AAB48185.1; PID:g514311
C:Superfamily: glucagon receptor
C:Keywords: G protein-coupled receptor; glycoprotein; intestine; transmembrane protei
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-459/Product: vasoactive intestinal polypeptide receptor #status predicted <MAT>
F:146-168/Domain: transmembrane #status predicted <TM1>
F:176-195/Domain: transmembrane #status predicted <TM2>
F:218-241/Domain: transmembrane #status predicted <TM3>
F:256-277/Domain: transmembrane #status predicted <TM4>
F:295-318/Domain: transmembrane #status predicted <TM5>
F:344-363/Domain: transmembrane #status predicted <TM6>
F:376-395/Domain: transmembrane #status predicted <TM7>
F:58,69,100,292/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 7.6e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
|||||
Db 171 LHCTRNYIHMLF 183

RESULT 11
JC2194
vasoactive intestinal peptide receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C:Accession: JC2194; JN0604; PC2289; S38397
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-Denis
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA en
A:Reference number: JC2194; MUID:94235025
A:Accession: JC2194
A:Molecule type: mRNA
A:Residues: 1-460 <COU>
A:Cross-references: EMBL:X75299; NID:9407461; PIDN:CAA53046.1; PID:9407462
A:Experimental source: jejunal epithelial cell; clone hIVR8
R:Sreedharan, S.P.; Patel, D.R.; Huang, J.X.; Goetzl, E.J.
Biochem. Biophys. Res. Commun. 193, 546-553, 1993
A:Title: Cloning and functional expression of a human neuroendocrine vasoactive intestinal
A:Reference number: JN0604; MUID:93290641
A:Accession: JN0604
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-284,288-460 <SRE>
A:Cross-references: GB:LJ3288; NID:9292903; PIDN:AAA36805.1; PID:g292904
R:Couvineau, A.; Gaudin, P.; Maoret, J.J.; Rouyer-Fessard, C.; Nicole, P.; Laburthe, M.
Biochem. Biophys. Res. Commun. 206, 246-252, 1995
A:Title: Highly conserved aspartate 68, tryptophane 73 and glycine 109 in the N-terminal
A:Reference number: PC2289; MUID:95118345
A:Accession: PC2289
A:Molecule type: mRNA
A:Residues: 63-129 <CO2>
C:Genetics:
A:Gene: GDB:VIPR1; RCD1; HVRI
A:Cross-references: GDB:128589; OMIM:192321
A:Map position: 3p22-3p22
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; hormone receptor; intestine; phosphoprotein; transmembrane pro
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-460/Product: vasoactive intestinal peptide receptor #status predicted <MAT>
F:145-168/Domain: transmembrane #status predicted <TM1>
F:176-194/Domain: transmembrane #status predicted <TM2>
F:216-234/Domain: transmembrane #status predicted <TM3>
F:253-277/Domain: transmembrane #status predicted <TM4>
F:299-319/Domain: transmembrane #status predicted <TM5>
F:346-363/Domain: transmembrane #status predicted <TM6>
F:377-396/Domain: transmembrane #status predicted <TM7>
F:58,69,100,293/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:76/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted
F:250/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:450/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

Query Match 2.4%; Score 13; DB 2; Length 460;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
|||||
Db 170 LHCTRNYIHMLF 182

RESULT 12
JC2462
gastric inhibitory polypeptide receptor - hamster
N:Alternate names: GIP receptor
C:Species: Cricetinae gen. sp. (hamster)
C:Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 20-Jun-2000

C:Accession: JC2462
R:Yasuda, K.; Inagaki, N.; Yamada, Y.; Kubota, A.; Seino, S.; Seino, Y.
Biochem. Biophys. Res. Commun. 205, 1556-1562, 1994
A:Title: Hamster gastric inhibitory polypeptide receptor expressed in pancreatic isle
A:Reference number: JC2462; MUID:95110292
A:Accession: JC2462
A:Molecule type: mRNA
A:Residues: 1-462 <YAS>
A:Cross-references: DDBJ:D38103; NID:9644880; PIDN:BAA07284.1; PID:g765087
C:Superfamily: glucagon receptor
C:Keywords: receptor; transmembrane protein
F:136-157/Domain: transmembrane #status predicted <TM1>
F:167-186/Domain: transmembrane #status predicted <TM2>
F:215-238/Domain: transmembrane #status predicted <TM3>
F:252-274/Domain: transmembrane #status predicted <TM4>
F:292-315/Domain: transmembrane #status predicted <TM5>
F:339-357/Domain: transmembrane #status predicted <TM6>
F:383-394/Domain: transmembrane #status predicted <TM7>

Query Match 2.4%; Score 13; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 7.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNYIHM 181
|||||
Db 159 FRLHCTRNYIHM 171

RESULT 13
JC2195
vasoactive intestinal peptide receptor-related protein precursor (clone hIVR5) - huma
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1995 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999
C:Accession: JC2195; S42087
R:Couvineau, A.; Rouyer-Fessard, C.; Darmoul, D.; Maoret, J.J.; Carrero, I.; Ogier-De
Biochem. Biophys. Res. Commun. 200, 769-776, 1994
A:Title: Human intestinal VIP receptor: cloning and functional expression of two cDNA
A:Reference number: JC2194; MUID:94235025
A:Accession: JC2195
A:Molecule type: mRNA
A:Residues: 1-495 <COU>
A:Cross-references: EMBL:X77777; NID:9456352; PIDN:CAA54814.1; PID:9456353
A:Experimental source: jejunal epithelial cell
C:Genetics:
A:Gene: GDB:VIPR1; RCD1; HVRI
A:Cross-references: GDB:128589; OMIM:192321
A:Map position: 3p22-3p22
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; intestine; phosphoprotein; receptor; transmembrane protein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-495/Product: vasoactive intestinal peptide receptor-related protein #status pred
F:180-203/Domain: transmembrane #status predicted <TM1>
F:211-229/Domain: transmembrane #status predicted <TM2>
F:251-269/Domain: transmembrane #status predicted <TM3>
F:290-312/Domain: transmembrane #status predicted <TM4>
F:334-354/Domain: transmembrane #status predicted <TM5>
F:381-398/Domain: transmembrane #status predicted <TM6>
F:412-431/Domain: transmembrane #status predicted <TM7>
F:93,104,135,328/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:111/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicte
F:285/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicte
F:485/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicte

Query Match 2.4%; Score 13; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 8.2e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMLF 184
|||||
Db 205 LHCTRNYIHMLF 217

RESULT 14

G02234
gastric inhibitory polypeptide receptor - human
N:Alternate names: GIP receptor
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C:Accession: G02234
R:Bonner, T.I.; Usdin, T.B.
submitted to the EMBL Data Library, October 1995
A:Reference number: G09336
A:Accession: G02234
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-466 <BON>
A:Cross-references: EMBL:U39231; NID:g1066050; PIDN:AAA84418.1; PID:g1066051
C:Genetics:
A:Gene: GDB:GIPR
A:Cross-references: GDB:335023
A:Map position: 19q13.3-19q13.3
C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180
|||||

Db 162 FRLHCTRNYYH 173

RESULT 15

S66676
glucose-dependent insulintropic protein receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S66676
R:Volz, A.; Goeke, R.; Lankat-Buttigereit, B.; Fehmann, H.C.; Bode, H.P.; Goeke, B.
FEBS Lett. 373, 23-29, 1995
A:Title: Molecular cloning, functional expression, and signal transduction of the GIP-receptor
A:Reference number: S66676; MUID:96013879
A:Accession: S66676
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-466 <VOL>
A:Cross-references: GB:S79852
A:Note: the authors translated the codon GCC for residue 427 as Leu
C:Superfamily: glucagon receptor
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-466/Product: glucose-dependent insulintropic protein receptor #status predicted <V

Query Match 2.2%; Score 12; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 0.00082;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180
|||||

Db 162 FRLHCTRNYYH 173

RESULT 16

I37411
glucose-dependent insulintropic polypeptide receptor - human
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
C:Accession: I37411
R:Gremlich, S.; Porret, A.; Hani, E.H.; Cherif, D.; Vionnet, N.; Froguet, P.; Thorens, B.
Diabetes 44, 1202-1208, 1995
A:Title: Cloning, functional expression, and chromosomal localization of the human pancreatic islet 1 gene
A:Reference number: I37411; MUID:96007224
A:Accession: I37411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-491 <RES>

A:Cross-references: EMBL:X81832; NID:g1030050; PIDN:CAA57426.1; PID:g1030051

C:Superfamily: glucagon receptor

Query Match 2.2%; Score 12; DB 2; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.00085;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRNYYH 180

|||||

Db 161 FRLHCTRNYYH 172

RESULT 17

JC2041
glucagon receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 28-May-1999
C:Accession: JC2041
R:MacNeil, D.J.; Occi, J.L.; Hey, P.J.; Strader, C.D.; Graziano, M.P.
Biochem. Biophys. Res. Commun. 198, 328-334, 1994
A:Title: Cloning and expression of a human glucagon receptor.
A:Reference number: JC2041; MUID:94121651
A:Accession: JC2041
A:Molecule type: mRNA
A:Residues: 1-477 <MAC>
A:Cross-references: GB:U03469; NID:g439689; PIDN:AAC52063.1; PID:g439690
C:Genetics:
A:Gene: GDB:GGR; GGR
A:Cross-references: GDB:304516; OMIM:138033
A:Map position: 17q25-17q25
C:Superfamily: glucagon receptor
C:Keywords: glycoprotein; receptor; transmembrane protein
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-477/Product: glucagon receptor #status predicted <MAT>
F:143-166/Domain: transmembrane #status predicted <TM1>
F:174-194/Domain: transmembrane #status predicted <TM2>
F:226-244/Domain: transmembrane #status predicted <TM3>
F:266-285/Domain: transmembrane #status predicted <TM4>
F:302-323/Domain: transmembrane #status predicted <TM5>
F:352-369/Domain: transmembrane #status predicted <TM6>
F:386-403/Domain: transmembrane #status predicted <TM7>
F:46-59,74,78/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.8%; Score 10; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYLHNL 264

|||||

Db 243 LVEGLYLHNL 252

Search completed: September 21, 2001, 17:10:40
Job time: 128 sec

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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:09:57 ; Search time 13.32 Seconds
(without alignments)
1391.308 Million cell updates/sec

Title: US-09-236-468A-2
Perfect score: 541
Sequence: 1 MAWLGLASLHWGWLMLGSL.....DDILMEKPSRPMSNPDETEG 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 93435 seqs, 34255486 residues

Word size : 10

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	363	67.1	550	1 PTH2_HUMAN	P49190 homo sapien
2	33	6.1	546	1 PTH2_RAT	P70555 rattus norv
3	25	4.6	585	1 PTHR_DIDNA	P25107 didelphis m
4	19	3.5	440	1 SCRC_HUMAN	P47872 homo sapien
5	19	3.5	449	1 SCRC_RAT	P23811 rattus norv
6	18	3.3	585	1 PTHR_PIG	P50133 sus scrofa
7	18	3.3	591	1 PTHR_MOUSE	P41593 mus musculus
8	18	3.3	591	1 PTHR_RAT	P25961 rattus norv
9	18	3.3	593	1 PTHR_HUMAN	Q03431 homo sapien
10	16	3.0	445	1 SCRC_RABIT	O46502 oryctolagus
11	16	3.0	447	1 VIPR_CARAU	Q90308 carassius a
12	13	2.4	455	1 GIPR_RAT	P43219 rattus norv
13	13	2.4	457	1 VIPR_HUMAN	P32241 homo sapien
14	13	2.4	458	1 VIPR_PIG	Q28992 sus scrofa
15	13	2.4	459	1 GIPR_PIG	P30083 rattus norv
16	13	2.4	462	1 GIPR_MESAU	P43218 mesocricetu
17	12	2.2	466	1 GIPR_HUMAN	P48546 homo sapien
18	10	1.8	477	1 GLR_HUMAN	P47871 homo sapien
19	10	1.8	550	1 GLP2_RAT	Q920W0 rattus norv
20	10	1.8	553	1 GLP2_HUMAN	O95838 homo sapien

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	550 AA.
PTH2_HUMAN				
ID	PTH2_HUMAN			
AC	P49190;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).			

GN PTHR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=95318121; PubMed=7797535;
RA Usdin T.B., Gruber C., Bonner T.I.;
RT "Identification and functional expression of a receptor selectively
recognizing parathyroid hormone, the PTH2 receptor.";
RL J. Biol. Chem. 270:15455-15458(1995).
RN [2]
RP SEQUENCE OF 26-40 AND 306-550 FROM N.A.
RX MEDLINE=97079671; PubMed=8921382;
RA Usdin T.B., Modi W., Bonner T.I.;
RT "Assignment of the human PTH2 receptor gene (PTH2R) to chromosome 2q33
by fluorescence in situ hybridization.";
RL Genomics 37:140-141(1996).
CC -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
ADENYL CYCLASE.
CC -!- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN AND PANCREAS.
CC ALSO EXPRESSED IN THE TESTIS.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL; U25128; AAC50157.1; -;
DR EMBL; U47124; AAA96796.1; -;
DR EMBL; U47129; AAC50767.1; -;
DR EMBL; U47125; AAC50767.1; JOINED.
DR EMBL; U47126; AAC50767.1; JOINED.
DR EMBL; U47127; AAC50767.1; JOINED.
DR EMBL; U47128; AAC50767.1; JOINED.
DR GCRDb; GCR_2003; -;
DR MIM; 601469; -;
DR InterPro; IPR000832; -;
DR Pfam; PF00002; 7tm2; 1
PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECP_F2_1; 1.
DR PROSITE; PS00550; G_PROTEIN_RECP_F2_2; 1.
DR PROSITE; PS00227; G_PROTEIN_RECP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 550
FT DOMAIN 27 145
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 169
FT DOMAIN 170 176
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 177 196
FT DOMAIN 197 237
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 260
FT DOMAIN 261 275
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 297
FT DOMAIN 298 316
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 317 337
FT DOMAIN 338 364
FT CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 365 383
FT DOMAIN 384 394
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 395 417
FT DOMAIN 418 550
FT CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 116 116
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 550 AA; 62235 MW; 2ADD14DBA68A9BF8 CRC64;

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Query Match          67.1%; Score 363; DB 1; Length 550;
Best Local Similarity 99.8%; Pred No. 0;
Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 LGASLHWGMLGSCLLARAQSDGTTTIERQIVLVKAKVOCELNITAQLQEGEGNC 63
DB 4 LGASLHWGMLGSCLLARAQSDGTTTIERQIVLVKAKVOCELNITAQLQEGEGNC 63

QY 64 FPEWGLICWPGTGVKISAVCPPIYDFNKHGVAFRCPNPGTWDFHSLNKTWANY 123
DB 64 FPEWGLICWPGTGVKISAVCPPIYDFNKHGVAFRCPNPGTWDFHSLNKTWANY 123

QY 124 DCLRFQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIHMHL 183
DB 124 DCLRFQPDISIGKQFCERLYVMYTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIHMHL 183

QY 184 FVSFMLRATSIYFVKDRVHAHIGVKELESIMODDPONSIEATSVDKSYIGCKIAVVMF 243
DB 184 FVSFMLRATSIYFVKDRVHAHIGVKELESIMODDPONSIEATSVDKSYIGCKIAVVMF 243

QY 244 IYFLATNYWILVEGLYLNHLIFVAFESDTKYLWGPFILGWGFPAAFAVAVARATLAD 303
DB 244 IYFLATNYWILVEGLYLNHLIFVAFESDTKYLWGPFILGWGFPAAFAVAVARATLAD 303

QY 304 ARCWLSAGDIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363
DB 304 ARCWLSAGDIKWIYQAPILAAIGLNFILFNTVRVLATKIWETNAVGHDTKQYRKLAK 363

QY 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCLEFFNSFGFFYSIIYCYNGEVAQE 423
DB 364 STLVLVLFVGVHYIVFVCLPHSFTGLGWIRHMCLEFFNSFGFFYSIIYCYNGEVAQE 423

QY 424 VKMWSRWNLSDVKRTPTCGSRRCGSVLTTVTHSTSSQVAA 467
DB 424 VKMWSRWNLSDVKRTPTCGSRRCGSVLTTVTHSTSSQVAA 467

RESULT 2
PTH2_RAT
ID PTH2_RAT STANDARD; PRT; 546 AA.
AC P70555;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PARATHYROID HORMONE RECEPTOR PRECURSOR (PTH2 RECEPTOR).
GN PTHR2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96426194; PubMed=8828488;
RA Usdin T.B., Bonner T.I., Harta G., Mezey E.;
RT "Distribution of parathyroid hormone-2 receptor messenger ribonucleic
RT acid in rat."
RL Endocrinology 137:4285-4297(1996).
CC -!- FUNCTION: THIS IS A SPECIFIC RECEPTOR FOR PARATHYROID HORMONE. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYL CYCLASE. PTHR2 MAY BE RESPONSIBLE FOR PTH EFFECTS IN A
CC NUMBER OF PHYSIOLOGICAL SYSTEMS. IT MAY PLAY A SIGNIFICANT ROLE IN
CC PANCREATIC FUNCTION. PTHR2 PRESENCE IN NEURONS INDICATES THAT IT
CC MAY FUNCTION AS A NEUROTRANSMITTER RECEPTOR.
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN BRAIN, ARTERIAL AND
CC CARDIAC ENDOTHELIUM. FOUND AS WELL IN SPERM, IN THE HEAD OF THE
CC EPIDIDYMIS. LOWER EXPRESSION IS FOUND IN VASCULAR SMOOTH MUSCLE,
CC EXOCRINE PANCREAS, TESTIS AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U55836; AAC52849.1; -.
CC GCRDb; GCR_1413; -.
CC InterPro; IPR000832; -.
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
CC PROSITE; PS00227; G_PROTEIN_RECEP_F2_3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24 POTENTIAL
FT CHAIN 25 546 PARATHYROID HORMONE RECEPTOR.
FT DOMAIN 27 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167 1 (POTENTIAL).
FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194 2 (POTENTIAL).
FT DOMAIN 195 235 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 236 258 3 (POTENTIAL).
FT DOMAIN 259 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 295 4 (POTENTIAL).
FT DOMAIN 296 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 334 5 (POTENTIAL).
FT DOMAIN 335 361 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 362 380 6 (POTENTIAL).
FT DOMAIN 381 391 7 (POTENTIAL).
FT TRANSMEM 392 414 7 (POTENTIAL).
FT DOMAIN 415 546 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 51 51 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 116 116 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 546 AA; 61800 MW; 2825AE4040313527 CRC64;

Query Match          6.1%; Score 33; DB 1; Length 546;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 YTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 180
DB 146 YTVGYSISFGSLAVAILIIGYFRRHLCHTRNYIH 178

RESULT 3
PTH2_RAT
ID PTHR2_DIDMA STANDARD; PRT; 585 AA.
AC P25107;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHR RECEPTOR).
GN PTHR.
OS Didelphis marsupialis virginiana (North American opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
OX NCBI_TaxID=9267;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92054592; PubMed=1658941;
RA Jueppner H., Abou-Samra A.-B., Freeman M., Kong X.-P., Schipani E.,
RA Richards J., Kolakowski L.F. Jr., Hock J., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "A G protein-linked receptor for parathyroid hormone and parathyroid
RT hormone-related peptide."
RL Science 254:1024-1026(1991).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
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FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 124 124 G -> A (IN REF. 1).
FT CONFLICT 210 210 A -> P (IN REF. 2).
FT CONFLICT 308 308 I -> F (IN REF. 3).
FT CONFLICT 333 333 E -> Q (IN REF. 3).
FT CONFLICT 377 377 G -> A (IN REF. 1).
SQ SEQUENCE 440 AA; 50206 MW; E22CDD0EE7C0ACC1 CRC64;

Query Match 3.5%; Score 19; DB 1; Length 440;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLFVSF 187
      |||||
Db 167 FRLHCTRYNIHMLFVSF 185
      |||||

RESULT 5
SCRC_RAT STANDARD; PRT; 449 AA.
AC P2381;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE SECRETIN RECEPTOR PRECURSOR (SCT-R).
GN SCTR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Nagata S.;
RX MEDLINE=91266890; PubMed=1646711;
RA Ishihara T., Nakamura S., Kaziro Y., Takahashi T., Takahashi K.,
RA Nagata S.;
RT "Molecular cloning and expression of a cDNA encoding the secretin
RT receptor.";
RL EMBO J. 10:1635-1641(1991).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; X59132; CAA41849.1; -.
CC DR PIR; S16319; S16319.
CC DR GCR0b; GCR_0242; -.
CC DR InterPro; IPR000832; -.
CC DR InterPro; IPR002144; -.
CC DR Pfam; PF00002; 7tm2; 1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR PRINTS; PR00490; SECRETINR.
CC DR PROSITE; PS00649; G_PROTEIN_RECP_F2.1; 1.
CC DR PROSITE; PS00650; G_PROTEIN_RECP_F2.2; 1.
CC DR PROSITE; PS0227; G_PROTEIN_RECP_F2.3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 22
FT CHAIN 23 449 POTENTIAL.
FT DOMAIN 23 143 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 167 1 (POTENTIAL).
FT DOMAIN 168 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 194 2 (POTENTIAL).
FT DOMAIN 195 216 EXTRACELLULAR (POTENTIAL).
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FT TRANSMEM 217 240 3 (POTENTIAL).
FT DOMAIN 241 254 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 255 276 4 (POTENTIAL).
FT DOMAIN 277 294 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 295 317 5 (POTENTIAL).
FT DOMAIN 318 343 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 344 362 6 (POTENTIAL).
FT TRANSMEM 363 392 7 (POTENTIAL).
FT DOMAIN 393 449 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 449 AA; 51234 MW; E70D05B5D061480D CRC64;

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLFVSF 187
      |||||
Db 167 FRLHCTRYNIHMLFVSF 185
      |||||

RESULT 6
PRTT_PIG STANDARD; PRT; 585 AA.
ID PRTT_PIG
AC P50133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTHr/PTHr RECEPTOR).
GN PTHRI OR PTHR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96303558; PubMed=8688470;
RA Black E.C., Smith D.P., Zhang X.Y., Frolik C.A., Harvey A.,
RA Chandrasekhar S., Hsiung H.M.;
RT "Structure and functional expression of a complementary DNA for
RT porcine parathyroid hormone/parathyroid hormone-related peptide
RT receptor.";
RL Biochim. Biophys. Acta 1307:339-347(1996).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; U18315; AAC48619.1; -.
CC DR GCR0b; GCR_1607; -.
CC DR InterPro; IPR000832; -.
CC DR InterPro; IPR002170; -.
CC DR Pfam; PF00002; 7tm2; 1.
CC DR PRINTS; PR00249; GPCRSECRETIN.
CC DR PRINTS; PR00393; PTHORMONER.
```


DR PROSITE; PS00649; G-PROTEIN_RECF_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECF_F2_2; 1.
DR PROSITE; PS00227; G-PROTEIN_RECF_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 585
FT DOMAIN 27 184
FT TRANSMEM 185 208
FT DOMAIN 209 215
FT TRANSMEM 216 235
FT DOMAIN 236 277
FT TRANSMEM 278 301
FT DOMAIN 302 315
FT TRANSMEM 316 337
FT DOMAIN 338 356
FT TRANSMEM 357 377
FT DOMAIN 378 404
FT TRANSMEM 405 423
FT DOMAIN 424 435
FT TRANSMEM 436 458
FT DOMAIN 459 585
FT CARBOHYD 147 147
FT CARBOHYD 157 157
FT CARBOHYD 162 162
FT CARBOHYD 172 172
SQ SEQUENCE 585 AA; 65682 MW; 60BE15CD49B7D210 CRC64;

Query Match 3.3%; Score 18; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYLH 262
DB 285 YFLATNYWILVEGLYLH 302

RESULT 7

PTRR_MOUSE STANDARD; PRT; 591 AA.
AC P41593; Q62119;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHR RECEPTOR).
GN PTHRI OR PTHR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HEHA;
RX MEDLINE=95034305; PubMed=7524627;
RA Karperien M., van Dijk T.B., Hoelmakers T., Cremers F.,
RA Abou-Samra A.-B., Boonstra J., de Laat S.W., Defize L.H.K.;
RT "Expression pattern of parathyroid hormone/parathyroid hormone
RT related peptide receptor mRNA in mouse postimplantation embryos
RT indicates involvement in multiple developmental processes.";
RN Mech. Dev. 47:29-42(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=94255468; PubMed=8197183;
RA McCuaig K.A., Clarke J.C., White J.H.;
RT "Molecular cloning of the gene encoding the mouse parathyroid
RT hormone/parathyroid hormone-related peptide receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:5051-5055(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL

CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
CC EMBL; X78936; CAA5536.1; -
DR EMBL; L34611; AAA40011.1; -
DR EMBL; L34608; AAA40011.1; JOINED.
DR EMBL; L34607; AAA40011.1; JOINED.
DR EMBL; L34609; AAA40011.1; JOINED.
DR EMBL; L34610; AAA40011.1; JOINED.
DR GCRDB; GCR_1005; -
DR GCRDB; GCR_1614; -
DR MGD; MGI:97801; Pthr.
DR InterPro; IPR000832; -
DR InterPro; IPR002170; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00649; G-PROTEIN_RECF_F2_1; 1.
DR PROSITE; PS00650; G-PROTEIN_RECF_F2_2; 1.
DR PROSITE; PS00227; G-PROTEIN_RECF_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 591
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 214 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 591
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT CARBOHYD 27 28
FT CONFLICT 464 465
FT CONFLICT 500 501
SQ SEQUENCE 591 AA; 66313 MW; F7876F8D388BDDFD CRC64;
RELATED PEPTIDE RECEPTOR.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
DA -> TS (IN REF. 2).
MISSING (IN REF. 2).
GA -> VS (IN REF. 2).

Query Match 3.3%; Score 18; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 245 YFLATNYWILVEGLYLH 262
DB 290 YFLATNYWILVEGLYLH 307

RESULT 8

PTRR_RAT STANDARD; PRT; 591 AA.
ID P25961;
AC P25961;
DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHrP RECEPTOR).
GN PTHrP OR PTHrP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Bone;
RX MEDLINE=92212903; PubMed=1313566;
RA Abou-Samra A.-B., Jueppner H., Force T., Freeman M.W., Kong X.-F.,
RA Schipani E., Urena P., Richards J., Bonventre J.V., Potts J.T. Jr.,
RA Kronenberg H.M., Segre G.V.;
RT "Expression cloning of a common receptor for parathyroid hormone and
RT parathyroid hormone-related peptide from rat osteoblast-like cells: a
RT single receptor stimulates intracellular accumulation of both cAMP
RT and inositol trisphosphates and increases intracellular free
RT calcium.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2732-2736(1992).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94292182; PubMed=8020952;
RA Pausova Z., Bourdon J., Clayton D., Mattel M.-G., Seldin M.F.,
RA Janicic N., Riviere M., Szpirer J., Levan G., Szpirer C.;
RT "Cloning of a parathyroid hormone/parathyroid hormone-related peptide
RT receptor (PTHrP) cDNA from a rat osteosarcoma (UMR 106) cell line:
RT chromosomal assignment of the gene in the human, mouse, and rat
RT genomes.";
RL Genomics 20:20-26(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR
CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER
CC SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M7184; AAA1811.1; -;
DR EMBL; L19475; AAA68098.1; -;
DR GCRDB; GCR_0206; -;
DR GCRDB; GCR_0938; -;
DR InterPro; IPR000832; -;
DR InterPro; IPR002170; -;
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 591
FT PARATHYROID HORMONE/PARATHYROID HORMONE-
FT RELATED PEPTIDE RECEPTOR.
FT EXTRACELLULAR (POTENTIAL).
FT 1 (POTENTIAL).
FT TRANSMEM 214 219
FT DOMAIN 214 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 591
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT SEQUENCE 591 AA; 66260 MW; 21944F3051B9E9C1 CRC64;
SQ
Query Match 3.3%; Score 18; DB 1; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 245 YFLATNYWILVEGLYLH 262
DB 290 YFLATNYWILVEGLYLH 307
|||||
RESULT 9
PTRR_HUMAN STANDARD; PRT; 593 AA.
AC Q03431;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PARATHYROID HORMONE/PARATHYROID HORMONE-RELATED PEPTIDE RECEPTOR
DE PRECURSOR (PTH/PTHrP RECEPTOR).
GN PTHrP OR PTHrP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=9338641; PubMed=8386612;
RA Schipani E., Karga H., Karaplis A.C., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
RT "Identical complementary deoxyribonucleic acids encode a human renal
RT and bone parathyroid hormone (PTH)/PTH-related peptide receptor.";
RL Endocrinology 132:2157-2165(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=93387403; PubMed=8397094;
RA Schneider H., Feyen J.-H., Rao Movva N.;
RT "Cloning and functional expression of a human parathyroid hormone
RT receptor.";
RL Eur. J. Pharmacol. 246:149-155(1993).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=95263723; PubMed=7745008;
RA Schipani E., Weinstein L.S., Bergwitz C., Iida-Klein A., Kong X.F.,
RA Stuhmann M., Kruse K., Whyte M.P., Murray T., Schmidtke J., Dop C.,
RA Brickman A.S., Crawford J.D., Potts J.T. Jr., Kronenberg H.M.,
RA Abou-Samra A.-B., Segre G.V., Jueppner H.;
RT "pseudohypoparathyroidism type 1b is not caused by mutations in the
RT coding exons of the human parathyroid hormone (PTH)/PTH-related
RT peptide receptor gene.";
RL J. Clin. Endocrinol. Metab. 80:1611-1621(1995).
RN [4]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Levine M.A.;
RN Submitted (xxx-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RN STRUCTURE BY NMR OF 168-198.
RX MEDLINE=98409426; PubMed=9737850;
RX Pellegrini M., Bisello A., Rosenblatt M., Chorev M., Mierke D.F.;

RT Binding domain of human parathyroid hormone receptor: from
RT conformation to function.;
RL Biochemistry 37:12737-12743(1998).

RN [6]

RP VARIANT MURK-JANSEN ARG-223.

RX MEDLINE-95215874; PubMed-7701349;

RA Schipani E., Kruse K., Juppner H.;

RT "A constitutively active mutant PTH-PTHrP receptor in Jansen-type

RT metaphyseal chondrodysplasia.";

RL Science 268:98-100(1995).

RN [7]

RP VARIANTS MURK-JANSEN ARG-223 AND PRO-410.

RX MEDLINE-96366745; PubMed-8703170;

RA Schipani E., Langman C.B., Parfitt A.M., Jensen G.S., Kikuchi S.,

RA Kooh S.W., Cole W.G., Juppner H.;

RT "Constitutively activated receptors for parathyroid hormone and

RT parathyroid hormone-related peptide in Jansen's metaphyseal

RT chondrodysplasia.";

RL New Engl. J. Med. 335:708-714(1996).

RN [8]

RP MUTAGENESIS OF ARG-223 AND PRO-410.

RX MEDLINE-97322091; PubMed-9178745;

RA Schipani E., Jensen G.S., Pincus J., Nissenson R.A., Gardella T.J.,

RA Juppner H.;

RT "Constitutive activation of the cyclic adenosine 3',5'-monophosphate

RT signaling pathway by parathyroid hormone (PTH)/PTHrP-related peptide

RT receptors mutated at the two loci for Jansen's metaphyseal

RT chondrodysplasia.";

RL Mol. Endocrinol. 11:851-858(1997).

CC [1]

CC -1- FUNCTION: THIS IS A RECEPTOR FOR PARATHYROID HORMONE AND FOR

CC PARATHYROID HORMONE-RELATED PEPTIDE. THE ACTIVITY OF THIS

CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL

CC CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER

CC SYSTEM.

CC [2]

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

CC -1- TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. MOST ABUNDANT IN

CC KIDNEY, BONE AND LIVER.

CC [3]

CC -1- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF BLOWSTRAND TYPE OF

CC CHONDRODYSPLASIA; A SEVERE SKELETAL DISPLASIA.

CC [4]

CC -1- DISEASE: DEFECTS IN PTHrP ARE THE CAUSE OF MURK-JANSEN TYPE OF

CC METAPHYSEAL CHONDRODYSPLASIA; A SEVERE SKELETAL DISPLASIA. IT IS

CC A RARE FORM OF SHORT-LIMBED DWARFISM ASSOCIATED WITH HYPERCALCEMIA

CC AND NORMAL OR LOW SERUM CONCENTRATIONS OF THE TWO PARATHYROID

CC HORMONES.

CC [5]

CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.

CC [6]

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CC [7]

CC EMBL; L04308; AAA36525.1; -

CC EMBL; X68596; CAA48589.1; -

CC EMBL; U22409; AAB60657.1; -

CC EMBL; U22401; AAB60657.1; JOINED.

CC EMBL; U22402; AAB60657.1; JOINED.

CC EMBL; U22403; AAB60657.1; JOINED.

CC EMBL; U22404; AAB60657.1; JOINED.

CC EMBL; U22405; AAB60657.1; JOINED.

CC EMBL; U22406; AAB60657.1; JOINED.

CC EMBL; U22407; AAB60657.1; JOINED.

CC EMBL; U22408; AAB60657.1; JOINED.

CC EMBL; U17418; AAA56774.1; -

CC PIR; S29610; S29610.

CC PIR; A49191; A49191.

CC PDB; 1BL1; 30-MAR-99.

CC GCRDB; GCR_0205; -

CC GCRDB; GCR_0647; -

CC GCRDB; GCR_1335; -

CC GCRDB; GCR_2025; -

DR MIM; 168468; -
DR MIM; 156400; -
DR MIM; 215045; -
DR InterPro; IPR000832; -
DR InterPro; IPR002170; -
DR Pfam; PF00002; 7Cm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00393; PTRHORMONER.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_4; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Disease mutation; 3D-structure.
FT SIGNAL 1 26
FT CHAIN 27 593
FT DOMAIN 27 188
FT TRANSMEM 189 212
FT DOMAIN 213 219
FT TRANSMEM 220 239
FT DOMAIN 240 282
FT TRANSMEM 283 306
FT DOMAIN 307 320
FT TRANSMEM 321 342
FT DOMAIN 343 361
FT TRANSMEM 362 382
FT DOMAIN 383 409
FT TRANSMEM 410 428
FT DOMAIN 429 440
FT TRANSMEM 441 463
FT DOMAIN 464 593
FT CARBOHYD 151 151
FT CARBOHYD 161 161
FT CARBOHYD 166 166
FT CARBOHYD 176 176
FT VARIANT 223 223
FT
FT VARIANT 410 410
FT
FT ACTIVATED
FT /FTID=VAR_003582.
FT T -> P (IN MURK JANSEN; CONSTITUTIVELY
FT ACTIVATED)
FT /FTID=VAR_003583.
FT K -> N (IN REF. 2).
FT S -> C (IN REF. 2).
SQ SEQUENCE 593 AA; 66360 MW; DA1400640A6C7F2B CRC64;

Query Match 3.3%; Score 18; DB 1; Length 593;
Best Local Similarity 100.0%; Pred. No. 2.8e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 245 YFLATNYWILVEGLYH 262
Db 290 YFLATNYWILVEGLYH 307
|||||

RESULT 10
SCRC_RABIT
ID SCRC_RABIT STANDARD; PRT; 445 AA.
AC 046502;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE SECRETIN RECEPTOR PRECURSOR (SCT-R).
GN SCTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBL_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-98366112; PubMed=9700755;
RA Svoboda M., Tastenoy M., de Neef P., Delporte C., Waelbroeck M.,
RA Robberecht P.;

RT "Molecular cloning and in vitro properties of the recombinant rabbit
 RT secretin receptor.";
 RL Peptides 19:1055-1062(1998).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR SECRETIN. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE.
 CC
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC
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 CC
 CC EMBL: AF025411; AAC32767.1; -.
 DR InterPro: IPR000832; -.
 DR InterPro: IPR001771; -.
 DR Pfam: PF002144; -.
 DR Pfam: PF00002; 7tm2; 1.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR PRINTS: PR00490; SECRETINR.
 DR PRINTS: PRO1134; VIPRECEPTOR.
 DR PROSITE: PS00649; G-PROTEIN_RECEP_F2_1; 1.
 DR PROSITE: PS00650; G-PROTEIN_RECEP_F2_2; 1.
 DR PROSITE: PS00651; G-PROTEIN_RECEP_F2_3; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 445
 FT DOMAIN 22 139
 FT TRANSMEM 140 163
 FT DOMAIN 164 170
 FT TRANSMEM 171 190
 FT DOMAIN 191 212
 FT TRANSMEM 213 236
 FT DOMAIN 237 250
 FT TRANSMEM 251 272
 FT DOMAIN 273 290
 FT TRANSMEM 291 313
 FT DOMAIN 314 339
 FT TRANSMEM 340 358
 FT DOMAIN 359 365
 FT TRANSMEM 366 388
 FT DOMAIN 389 445
 FT CARBOHYD 68 68
 FT CARBOHYD 96 96
 FT CARBOHYD 102 102
 FT CARBOHYD 124 124
 FT SEQUENCE 445 AA; 50495 MW; 31C4169CB099F194 CRC64;

Query Match 3.0%; Score 16; DB 1; Length 445;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRYNIHMLF 184
 |||||
 Db 163 FRLHCTRYNIHMLF 178

RESULT 11
 VIPR_CARAU
 ID VIPR_CARAU STANDARD; PRT; 447 AA.
 AC Q90308;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR).
 OS Carassius auratus (Goldfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Cyprininae; Carassius.
 RN NCBI_TaxID=7957;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190233; PubMed=9038250;
 RA Chow B.K.C., Yuen T.T.H., Chan K.W.;
 RT "Molecular evolution of vertebrate VIP receptors and functional
 RT characterization of a VIP receptor from goldfish Carassius auratus.";
 RL Gen. Comp. Endocrinol. 105:176-185(1997).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE.
 CC
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC
 CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
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 CC
 CC EMBL: U56391; AAB05459.1; -.
 DR GCRDb; GCR_1205; -.
 DR InterPro; IPR000832; -.
 DR Pfam: PF00002; 7tm2; 1.
 DR PRINTS: PR00249; GPCRSECRETIN.
 DR PROSITE: PS00649; G-PROTEIN_RECEP_F2_1; 1.
 DR PROSITE: PS00650; G-PROTEIN_RECEP_F2_2; 1.
 DR PROSITE: PS00651; G-PROTEIN_RECEP_F2_3; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 103
 FT TRANSMEM 104 128
 FT DOMAIN 129 135
 FT TRANSMEM 136 155
 FT DOMAIN 156 178
 FT TRANSMEM 179 202
 FT DOMAIN 203 216
 FT TRANSMEM 217 238
 FT DOMAIN 239 255
 FT TRANSMEM 257 280
 FT DOMAIN 281 305
 FT TRANSMEM 306 325
 FT DOMAIN 326 337
 FT TRANSMEM 338 357
 FT DOMAIN 358 447
 FT CARBOHYD 17 17
 FT CARBOHYD 22 22
 FT CARBOHYD 64 64
 FT CARBOHYD 91 91
 FT CARBOHYD 169 169
 FT SEQUENCE 447 AA; 50959 MW; 66839E243702554C CRC64;

Query Match 3.0%; Score 16; DB 1; Length 447;
 Best Local Similarity 100.0%; Pred. No. 2.5e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNIHMLFVSF 187
 |||||
 Db 131 LHCTRYNIHMLFVSF 146

RESULT 12
 GIPR_RAT
 ID GIPR_RAT STANDARD; PRT; 455 AA.
 AC P43219;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-
 DE DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).

GN OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Brain;
RX MEDLINE=94062667; PubMed=8243312;
RA Usdin T.B., Mezey E., Button D.C., Brownstein M.J., Bonner T.I.;
RT "Gastric inhibitory polypeptide receptor, a member of the secretin-
vasoactive intestinal peptide receptor family, is widely distributed
in peripheral organs and the brain.";
RL Endocrinology 133:2861-2871(1993).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
CYCLASE.
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CYCLASE.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- TISSUE SPECIFICITY: PRESENT IN THE PANCREAS AS WELL AS THE GUT,
ADIPOSE TISSUE, HEART, PITUITARY, AND INNER LAYERS OF THE ADRENAL
CORTEX, WHEREAS IT IS NOT FOUND IN KIDNEY, SPLEEN, OR LIVER. IT IS
CC ALSO EXPRESSED IN SEVERAL BRAIN REGIONS, INCLUDING THE CEREBRAL
CORTEX, HIPPOCAMPUS, AND OLFACTORY BULB.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL: L19660; AAC37637.1; -
CC CCRdb; GCR_0817; -
CC InterPro; IPR000832; -
CC InterPro; IPR001749; -
CC Pfam; PF00002; 7tm_2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PROSITE; PR01129; GIPRECEPTIN.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00651; G_PROTEIN_RECEP_F2_3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
CC SIGNAL 1 18
FT CHAIN 19 455
FT DOMAIN 19 135
FT TRANSMEM 136 158
FT DOMAIN 159 166
FT TRANSMEM 167 186
FT DOMAIN 187 214
FT TRANSMEM 215 239
FT DOMAIN 240 251
FT TRANSMEM 252 275
FT DOMAIN 276 290
FT TRANSMEM 291 316
FT DOMAIN 317 338
FT TRANSMEM 339 359
FT DOMAIN 360 374
FT TRANSMEM 375 395
FT DOMAIN 396 455
FT CARBOHYD 59 69
FT CARBOHYD 69 79
FT CARBOHYD 74 74
CC SEQUENCE 455 AA; 52256 MW; 5454B0638ABF9A06 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 455;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 169 FRRLHCTRYNIHM 181
|||||

DB 159 FRRLHCTRYNIHM 171
RESULT 13
VIPR_HUMAN
ID VIPR_HUMAN STANDARD: PRT; 457 AA.
AC P32241; Q15871;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93290641; PubMed=8390245;
RA Sreedharan S.P., Patel D.R., Huang J.-X., Goetzl E.J.;
RT "Cloning and functional expression of a human neuroendocrine
vasoactive intestinal peptide receptor.";
RL Biochem. Biophys. Res. Commun. 193:546-553(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=94235025; PubMed=8179610;
RA Couvineau A., Rouyer-Fessard C., Darmoul D., Maoret J.J., Carrero I.,
Ogier-Denis E., Laburthe M.;
RT "Human intestinal VIP receptor: cloning and functional expression of
two cDNA encoding proteins with different N-terminal domains.";
RL Biochem. Biophys. Res. Commun. 200:769-776(1994).
RN [3]
RP SEQUENCE OF 33-457 FROM N.A.
RX MEDLINE=95001220; PubMed=7917790;
RA Gagnon A.W., Aiyar N., Elshourbagy N.A.;
RT "Molecular cloning and functional characterization of a human liver
vasoactive intestinal peptide receptor.";
RL Cell. Signal. 6:321-333(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYL
CYCLASE. THE AFFINITY IS VIP = PACAP-27 > PACAP-38.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING.
CC -!- TISSUE SPECIFICITY: IN LUNG, HT29 COLONIC EPITHELIAL CELLS,
RAJI B-LYMPHOBLASTS. LESSER EXTENT IN BRAIN, HEART, KIDNEY,
LIVER AND PLACENTA.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL: U11087; AAB60362.1; -
CC EMBL: U11079; AAB60362.1; JOINED.
CC EMBL: U11080; AAB60362.1; JOINED.
CC EMBL: U11081; AAB60362.1; JOINED.
CC EMBL: U11083; AAB60362.1; JOINED.
CC EMBL: U11084; AAB60362.1; JOINED.
CC EMBL: U11085; AAB60362.1; JOINED.
CC EMBL: U11086; AAB60362.1; JOINED.
CC EMBL: L13288; AAA36805.1; -
CC EMBL: X77777; CAA54814.1; -
CC EMBL: X75299; CAA53046.1; -

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DR EMBL; L20295; AAA36802.1; -.
DR PIR; JN0604; JN0604.
DR GCRDB; GCR_0397; -.
DR GCRDB; GCR_0652; -.
DR GCRDB; GCR_0774; -.
DR GCRDB; GCR_0904; -.
DR GCRDB; GCR_1886; -.
DR MIM; 192321; -.
DR InterPro; IPR000832; -.
DR InterPro; IPR001571; -.
DR InterPro; IPR001771; -.
DR Pfam; PF00002; 7tm2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PRINTS; PR00491; VASOACTIVEIPR.
DR PRINTS; PR01154; VIPRECEPTOR.
DR PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
DR PROSITE; PS0227; G_PROTEIN_RECF_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 31 457
FT VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 1.
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 31 142
FT TRANSMEM 143 167
FT DOMAIN 168 174
FT TRANSMEM 175 194
FT DOMAIN 195 216
FT TRANSMEM 217 240
FT DOMAIN 241 254
FT TRANSMEM 255 276
FT DOMAIN 277 292
FT TRANSMEM 293 316
FT DOMAIN 317 341
FT TRANSMEM 342 361
FT DOMAIN 362 373
FT TRANSMEM 374 393
FT DOMAIN 394 457
FT CARBOHYD 58 58
FT CARBOHYD 69 69
FT CARBOHYD 100 100
FT CARBOHYD 290 290
FT VARSPPLIC 1 32
FT SEQUENCE 457 AA; 51547 MW; DAA40CF5BEC47D7D CRC64;

Query Match 2.4%; Score 13; DB 1; Length 457;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
DB 170 LHCTRNVIHMLF 182
|||||

RESULT 14
VIPR_PIG STANDARD; PRT; 458 AA.
AC Q28992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR I PRECURSOR (VIP-R-1)
DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
GN VIPR1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]

```

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RP SEQUENCE FROM N.A.
RA Hsiung H.M., Smith D.P., Hyslop P.A., Helman M.L., Hassan H.A.,
RA Zhang X.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC !- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
CC CYCLASE (BY SIMILARITY).
CC !- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC !- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U49434; AAA93390.1; -.
CC GCRDB; GCR_1565; -.
CC InterPro; IPR000832; -.
CC InterPro; IPR001571; -.
CC InterPro; IPR001771; -.
CC Pfam; PF00002; 7tm2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PRINTS; PR00491; VASOACTIVEIPR.
CC PRINTS; PR01154; VIPRECEPTOR.
CC PROSITE; PS00649; G_PROTEIN_RECF_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECF_F2_2; 1.
CC PROSITE; PS0227; G_PROTEIN_RECF_F2_3; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 31
FT CHAIN 32 458
FT VASOACTIVE INTESTINAL POLYPEPTIDE
FT RECEPTOR 1.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 144 168
FT DOMAIN 169 175
FT TRANSMEM 176 195
FT DOMAIN 196 217
FT TRANSMEM 218 241
FT DOMAIN 242 255
FT TRANSMEM 256 277
FT DOMAIN 278 293
FT TRANSMEM 294 317
FT DOMAIN 318 342
FT TRANSMEM 343 362
FT DOMAIN 363 374
FT TRANSMEM 375 394
FT DOMAIN 395 458
FT CARBOHYD 59 59
FT CARBOHYD 70 70
FT CARBOHYD 101 101
FT CARBOHYD 105 105
FT SEQUENCE 458 AA; 51479 MW; E166E4D6B3BE1189 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
DB 171 LHCTRNVIHMLF 183
|||||

RESULT 15
VIPR_RAT STANDARD; PRT; 459 AA.
AC P30083;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR I PRECURSOR (VIP-R-1)

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DE (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE II RECEPTOR)
 DE (PACAP TYPE II RECEPTOR) (PACAP-R-2).
 GN VIPR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=92232309; PubMed=1314625;
 RA Ishihara T., Shigemoto R., Mori K., Takahashi K., Nagata S.;
 RT "Functional expression and tissue distribution of a novel receptor
 RT for vasoactive intestinal polypeptide.";
 RL Neuron 8:811-819(1992).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: IN LIVER, LUNG, INTESTINES, THYMUS AND BRAIN
 CC (MOSTLY IN THE CEREBRAL CORTEX AND HIPPOCAMPUS).
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; M86835; AAA42331.1; -;
 DR PIR; JH0594; JH0594.
 DR GCRDB; GCR_0369; -;
 DR InterPro; IPR000832; -;
 DR InterPro; IPR001571; -;
 DR InterPro; IPR001771; -;
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PRINTS; PR00491; VASOACTIVEIPR.
 DR PRINTS; PR01154; VIP1RECEPTOR.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL
 FT CHAIN 1 30
 FT CHAIN 31 459
 FT RECEPTOR 1.
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 31 143
 FT TRANSMEM 144 168
 FT DOMAIN 169 175
 FT TRANSMEM 176 195
 FT DOMAIN 196 217
 FT TRANSMEM 218 241
 FT DOMAIN 242 255
 FT TRANSMEM 256 277
 FT DOMAIN 278 294
 FT TRANSMEM 295 318
 FT DOMAIN 319 343
 FT TRANSMEM 344 363
 FT DOMAIN 364 375
 FT TRANSMEM 376 395
 FT DOMAIN 396 459
 FT CARBOHYD 58 58
 FT CARBOHYD 69 69
 FT CARBOHYD 100 100
 FT CARBOHYD 292 292
 FT SEQUENCE 459 AA; 52057 MW; 99E8957DA86698D2 CRC64;

Query Match 2.48; Score 13; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 3.1e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRYNIHMLF 184
 DB 171 LHCTRYNIHMLF 183
 RESULT 16
 ID GIPR_MESAU STANDARD; PRT; 462 AA.
 AC P43218;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-
 DE DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
 GN GIPR.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95110292; PubMed=7811236;
 RA Yasuda K., Inagaki N., Yamada Y., Kubota A., Seino S., Seino Y.;
 RT "Hamster gastric inhibitory polypeptide receptor expressed in
 RT pancreatic islets and clonal insulin-secreting cells: its structure
 RT and functional properties.";
 RL Biochem. Biophys. Res. Commun. 205:1556-1562(1994).
 CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
 CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLIL
 CC CYCLASE.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY DISTRIBUTED INCLUDING PANCREATIC
 CC ISLETS, BRAIN AND VARIOUS PERIPHERAL TISSUES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL; D38103; BAA07284.1; -;
 DR GCRDB; GCR_1162; -;
 DR InterPro; IPR000832; -;
 DR InterPro; IPR001749; -;
 DR Pfam; PF00002; 7tm_2; 1.
 DR PRINTS; PR00249; GPCRSECRETIN.
 DR PRINTS; PR01129; GIPRECEPTOR.
 DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
 DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
 DR PROSITE; PS0227; G_PROTEIN_RECEP_F2_3; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Signal.
 KW SIGNAL
 FT CHAIN 1 18
 FT CHAIN 19 462
 FT DOMAIN 19 135
 FT TRANSMEM 136 158
 FT DOMAIN 159 166
 FT TRANSMEM 167 186
 FT DOMAIN 187 214
 FT TRANSMEM 215 239
 FT DOMAIN 240 251
 FT TRANSMEM 252 275
 FT DOMAIN 276 290
 FT TRANSMEM 291 316
 FT DOMAIN 317 338
 FT TRANSMEM 339 359
 FT DOMAIN 360 374
 FT TRANSMEM 375 395
 FT DOMAIN 396 462
 FT GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR.
 FT EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 5 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 6 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 7 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 462


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FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 74 74 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 462 AA; 52918 MW; D7A6204BCB9BB688 CRC64;

Query Match 2.4%; Score 13; DB 1; Length 462;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRLHCTRNVIHM 181
Db 159 FRLHCTRNVIHM 171

RESULT 17
GIPR_HUMAN STANDARD; PRT; 466 AA.
ID GIPR_HUMAN STANDARD; PRT; 466 AA.
AC P48346; Q16400; Q14401;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE GASTRIC INHIBITORY POLYPEPTIDE RECEPTOR PRECURSOR (GIP-R) (GLUCOSE-
DE DEPENDENT INSULINOTROPIC POLYPEPTIDE RECEPTOR).
GN GIPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Usdin T.B., Gruber C., Modi W., Bonner T.I.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RX MEDLINE=96013879; PubMed=7589426;
RA Volz A., Goke R., Lankat-Buttgereit B., Fehmann H.C., Bode H.P.,
RA Goke B.;
RT "Molecular cloning, functional expression, and signal transduction of
RT the GIP-receptor cloned from a human insulinoma.";
RL FEBS Lett. 373:23-29(1995).
RN [3]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP TISSUE=Pancreas;
RX MEDLINE=96007224; PubMed=7556958;
RA Greulich S., Porret A., Hani E.H., Cherif D., Vionnet N., Froguel P.,
RA Thorens B.;
RT "Cloning, functional expression, and chromosomal localization of the
RT human pancreatic islet glucose-dependent insulinotropic polypeptide
RT receptor.";
RL Diabetes 44:1202-1208(1995).
RN [4]
SEQUENCE FROM N.A.
RX MEDLINE=96121393; PubMed=8575774;
RA Yamada Y., Hayami T., Nakamura K., Kaisaki P.J., Someya Y.,
RA Wang C.Z., Seino S., Seino Y.;
RT "Human gastric inhibitory polypeptide receptor: cloning of the gene
RT (GIPR) and cDNA.";
RL Genomics 29:773-776(1995).
RN [5]
SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala N., Terry A., Garnes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and
RT D19S412.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR GIP. THE ACTIVITY OF THIS
CC RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE ADENYLYL
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RESULT 18
GLR_HUMAN
ID GLR_HUMAN STANDARD; PRT; 477 AA.
AC P47871;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GLUCAGON RECEPTOR PRECURSOR (GL-R).
DE GPCR.
GN GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=94121651; PubMed=7507321;
RA Macneil D.J., Occi J.L., Hey P.J., Strader C.D., Graziano M.P.;
RT "Cloning and expression of a human glucagon receptor.";
RT Biochem. Biophys. Res. Commun. 198;328-334(1994).
RL Gene 140:203-209(1994).
RN [3]
RP VARIANT SER-40.
RX MEDLINE=96034210; PubMed=7589886;
RX Fujisawa T., Ikegami H., Yamato E., Takekawa K., Nakagawa Y.,
RA Hamada Y., Ueda H., Fukuda M., Ogiwara T.;
RT "A mutation in the glucagon receptor gene (Gly40Ser): heterogeneity
in the association with diabetes mellitus.";
RL Diabetologia 38:983-985(1995).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR GLUCAGON WHICH PLAYS A CENTRAL
CC ROLE IN REGULATING THE LEVEL OF BLOOD GLUCOSE BY CONTROLLING THE
CC RATE OF HEPATIC GLUCOSE PRODUCTION AND INSULIN SECRETION. THE
CC ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
CC ADENYL CYCLASE AND ALSO A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
CC MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- DISEASE: IT IS A CANDIDATE FOR CERTAIN DEFECTS IN NON-INSULIN-
CC DEPENDENT DIABETES MELLITUS (NIDDM). THE VARIANT IN POSITION 40
CC (SER) IS FOUND IN SOME NIDDM PATIENTS, BUT ALSO IN NONDIABETIC
CC SUBJECTS.
CC -!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; U03469; AAC52063.1; -
CC EMBL; L20316; AAA53628.1; -
CC GCRDB; GCR_0772; -
CC GCRDB; GCR_0881; -
CC MIN; 138033; -
CC InterPro; IPR000832; -
CC Pfam; PF00002; 7tm.2; 1.
CC PRINTS; PR00249; GPCRSECRETIN.
CC PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
CC PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;
KW Polymorphism; Diabetes.
FT SIGNAL 1 25
POTENTIAL.
us-09-236-468a-2.olilo.rsp
Page 13
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:10:17 ; Search time 27.75 Seconds
(without alignments)
2579.352 Million cell updates/sec

Title: US-09-236-468A-2
Perfect score: 541
Sequence: 1 MAWLGLASLHVWGLMLGSL.....DDILMKPSPMESNPDTEG 541
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 425026 seqs, 132305027 residues
Word size : 10
Total number of hits satisfying chosen parameters: 12
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 1000 summaries

Database : SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mhbc:*
7: sp_mhbc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	7.0	169	11 Q9R1D4	Q9r1d4 mus musculus
2	27	5.0	173	13 Q9PWB7	Q9pwb7 brachydanio
3	20	3.7	94	13 Q9PRG1	Q9prg1 ictalurus p
4	18	3.3	536	13 Q9PVD3	Q9pvd3 brachydanio
5	18	3.3	595	6 Q9TU31	Q9tu31 canis famli
6	13	2.4	418	13 Q9IBG2	Q9ibg2 gallus gall
7	13	2.4	444	13 Q9YHC6	Q9yhc6 rana ridibu
8	13	2.4	459	11 Q9J1T8	Q9j1t8 mus musculu
9	13	2.4	459	11 Q9J1T0	Q9j1t0 mus musculu
10	11	2.0	542	13 Q9PVD2	Q9pvd2 brachydanio
11	10	1.8	48	11 Q9J1Y4	Q9j1y4 mus musculu
12	10	1.8	167	13 Q9YHC8	Q9yhc8 rana ridibu

ALIGNMENTS

RESULT 1
Q9R1D4

ID Q9R1D4 PRELIMINARY; PRT; 169 AA.
AC Q9R1D4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132083; AAD51909.1; -
DR InterPro; IPR000832; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
KW Receptor.
FT NON_TER 1 169
FT NON_TER 169 169
SQ SEQUENCE 169 AA; 19674 MW; 748CC8231FC69EA CRC64;

Query Match 7.0%; Score 38; DB 11; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.9e-30;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 316 WIYQAPILAAIGLNFILNTVRLATKIWTNAVCHD 353
DB 66 WIYQAPILAAIGLNFILNTVRLATKIWTNAVCHD 103

RESULT 2

Q9PWB7
ID Q9PWB7 PRELIMINARY; PRT; 575 AA.
AC Q9PWB7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=99367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RL J. Biol. Chem. 274:23035-23042(1999).
DR EMBL; AF132082; AAD51908.1; -
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
SQ SEQUENCE 575 AA; 64244 MW; 888F1C4DDB3A14DC CRC64;

```
Query Match          5.0%; Score 27; DB 13; Length 575;
Best Local Similarity 100.0%; Pred. No. 9.8e-19;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 IIGYFRLHCTRNYYIHMLHVSFMLRA 191
      |||||
Db 193 IIGYFRLHCTRNYYIHMLHVSFMLRA 219

RESULT 3
Q9PRG1 ID Q9PRG1 PRELIMINARY; PRT; 94 AA.
AC Q9PRG1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE TYPE-2 RECEPTOR PRECURSOR (FRAGMENT).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Siluriformes; Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, AND LIVER;
RX MEDLINE=9367425; PubMed=10438471;
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RT "A G protein-coupled receptor from zebrafish is activated by human
parathyroid hormone and not by human or teleost parathyroid hormone-
related peptide. Implications for the evolutionary conservation of
calcium-regulating peptide hormones.";
RT J. Biol. Chem. 274:23035-23042(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Rubin D.A., Hellman P., Zon L.I., Lobb C.J., Bergwitz C., Juppner H.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF132081; AAD51907.1; -.
DR EMBL; AF132078; AAD51906.1; -.
DR EMBL; AF132079; AAD51906.1; JOINED.
DR EMBL; AF132080; AAD51906.1; JOINED.
DR InterPro; IPR000832; -.
DR InterPro; IPR001211; -.
DR PRINTS; PR00249; GPCRSECRETIN.
DR ProDom; PD000303; -. 1.
KW Receptor.
FT NON_TER 1 94
FT SEQUENCE 94 AA; 10729 MW; D949182E1D2613EF CRC64;

Query Match          3.7%; Score 20; DB 13; Length 94;
Best Local Similarity 100.0%; Pred. No. 2.9e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 243 FIYFLATNYYWILVEGLYLH 262
      |||||
Db 10 FIYFLATNYYWILVEGLYLH 29

RESULT 4
Q9PVD3 ID Q9PVD3 PRELIMINARY; PRT; 536 AA.
AC Q9PVD3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE RECEPTOR PTH1R.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;

Query Match          3.3%; Score 18; DB 13; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99428481; PubMed=10497171;
RA Rubin D.A., Juppner H.;
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-
related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is
Preferentially Activated by Mammalian and Fuguish Parathyroid
Hormone-related Peptide.";
RT J. Biol. Chem. 274:28185-28190(1999).
DR EMBL; AF132084; AAF01265.1; -.
DR HSP; Q03431; IBL1.
DR InterPro; IPR000832; -.
DR InterPro; IPR001879; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEPTOR_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 536 AA; 61454 MW; 653B0A56DB2C8FA9 CRC64;

Query Match          3.3%; Score 18; DB 13; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.5e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 167 GYFRRLLHCTRNYYIHMLH 184
      |||||
Db 167 GYFRRLLHCTRNYYIHMLH 184

RESULT 5
Q9TU31 ID Q9TU31 PRELIMINARY; PRT; 595 AA.
AC Q9TU31;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PARATHYROID HORMONE RECEPTOR-1.
RN PTH1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Smock S.L., Vogt G.A., Castleberry T.A., Lu B., Owen T.A.;
RT "Molecular cloning and functional characterization of the canine
parathyroid hormone receptor-1 (PTH1).";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF167095; AAD55938.1; -.
DR HSP; Q03431; IBL1.
DR InterPro; IPR000832; -.
DR InterPro; IPR001879; -.
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEPTOR_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEPTOR_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 595 AA; 66308 MW; 09568ECF38D4D258 CRC64;

Query Match          3.3%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 YFLATNYYWILVEGLYLH 262
      |||||
Db 289 YFLATNYYWILVEGLYLH 306
```

```
RESULT 6
Q9IBG2 ID Q9IBG2 PRELIMINARY; PRT; 418 AA.
AC Q9IBG2;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-WAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR (FRAGMENT).
GN CVIPR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kansaku N., Shimada K., Saito N., Arakawa K., Suzuki T., Matsuda Y.,
RA Zadvorny D.;
RT "Molecular cloning of chicken VIP receptor cDNA, tissue distribution
RT and chromosomal localization."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029895; BAA95164.1; -
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 418 AA; 48191 MW; 7AE4796ADC08FF3 CRC64;

Query Match 2.4%; Score 13; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMHLF 184
DB 130 LHCTRNYIHMHLF 142
|||||
DB 130 LHCTRNYIHMHLF 142

RESULT 7
Q9YHC6 ID Q9YHC6 PRELIMINARY; PRT; 444 AA.
AC Q9YHC6;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE/PITUITARY ADENYLATE CYCLASE ACTIVATING
DE POLYPEPTIDE RECEPTOR.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RA Alexandre D., Anouar Y.;
RA "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue
RT distribution characteristics of both VPAC1 and VPAC2 receptors in
RT mammals."
RL Endocrinology 0:0-0(1999).
DR EMBL; AF100644; AAD03602.1; -
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
```

```
SQ SEQUENCE 444 AA; 50955 MW; 883B25B729314C4C CRC64;

Query Match 2.4%; Score 13; DB 13; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMHLF 184
DB 157 LHCTRNYIHMHLF 169
|||||
DB 157 LHCTRNYIHMHLF 169

RESULT 8
Q9RIT8 ID Q9RIT8 PRELIMINARY; PRT; 459 AA.
AC Q9RIT8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-WAR-2001 (TREMBlrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL POLYPEPTIDE 1 (VPAC1) RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hashimoto H., Nishino A., Shintani N., Hagihara N., Copeland N.G.,
RA Jenkins N.A., Yamamoto K., Matsuda T., Ishihara T., Nagata S.,
RA Baba A.;
RT "Genomic organization and chromosomal location of the mouse vasoactive
RT intestinal polypeptide 1 (VPAC1) receptor."
RL Genomics 58:90-93(1999).
DR EMBL; AB022860; BAA81896.1; -
DR EMBL; AB022848; BAA81896.1; JOINED.
DR EMBL; AB022849; BAA81896.1; JOINED.
DR EMBL; AB022850; BAA81896.1; JOINED.
DR EMBL; AB022851; BAA81896.1; JOINED.
DR EMBL; AB022852; BAA81896.1; JOINED.
DR EMBL; AB022853; BAA81896.1; JOINED.
DR EMBL; AB022854; BAA81896.1; JOINED.
DR EMBL; AB022855; BAA81896.1; JOINED.
DR EMBL; AB022856; BAA81896.1; JOINED.
DR EMBL; AB022857; BAA81896.1; JOINED.
DR EMBL; AB022858; BAA81896.1; JOINED.
DR EMBL; AB022859; BAA81896.1; JOINED.
DR InterPro; IPR000832; -
DR InterPro; IPR001879; -
DR Pfam; PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; HormR; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52094 MW; C0C3A9AE1ADF611D CRC64;

Query Match 2.4%; Score 13; DB 13; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNYIHMHLF 184
DB 171 LHCTRNYIHMHLF 183
|||||
DB 171 LHCTRNYIHMHLF 183

RESULT 9
Q9J140 ID Q9J140 PRELIMINARY; PRT; 459 AA.
AC Q9J140;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
```

DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VASOACTIVE INTESTINAL PEPTIDE RECEPTOR TYPE 1.
GN VIPR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RA Karacay B., O'Dorisio M.S., Kasow K., Krahe R.;
RT "Cloning and Fine Mapping of the Vasoactive Intestinal Peptide
RT Receptor I (VPAC1): A Comparative Analysis of Human, Rat and Murine
RT genes.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF266282; AAF77053.1; -.
DR InterPro: IPR000832; -.
DR Pfam: PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 459 AA; 52095 MW; 9D1ADF8567D4D7F CRC64;

Query Match 2.4%; Score 13; DB 11; Length 459;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHMLF 184
Db 171 LHCTRNVIHMLF 183

RESULT 10
Q9PVD2 ID Q9PVD2 PRELIMINARY; PRT; 542 AA.
AC Q9PVD2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE PARATHYROID HORMONE-RELATED PROTEIN RECEPTOR PTH3R.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Rasbora; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-99428481; PubMed=10497171;
RA Rubin D.A., Jueppner H.;
RT "Zebrafish Express the Common Parathyroid Hormone/Parathyroid Hormone-
RT related Peptide Receptor (PTH1R) and a Novel Receptor (PTH3R) That Is
RT Preferentially Activated by Mammalian and Fuguish Parathyroid
RT Hormone-related Peptide.";
RL J. Biol. Chem. 274:28185-28190(1999).
DR EMBL: AF132085; AAF01266.2; -.
DR InterPro: IPR000832; -.
DR InterPro: IPR001879; -.
DR Pfam: PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
DR SMART; SM00008; Hormr; 1.
KW Receptor.
SQ SEQUENCE 542 AA; 61438 MW; 08688658E2727303 CRC64;

Query Match 2.0%; Score 11; DB 13; Length 542;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 YWILVEGLYLH 262
Db 236 YWILVEGLYLH 246

RESULT 11
Q9JIY4 ID Q9JIY4 PRELIMINARY; PRT; 48 AA.
AC Q9JIY4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCAGON-LIKE PEPTIDE 2 RECEPTOR PRECURSOR (FRAGMENT).
GN GLP2R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWR/J; TISSUE=SMALL INTESTINE;
RA Bjerknes M., Cheng H.;
RT "Clonal analysis of the effects of glucagon-like peptide 2 (GLP-2) and
RT keratinocyte growth factor (KGF) on mouse intestinal epithelial
RT progenitors.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF166265; AAF89584.1; -.
DR InterPro: IPR000832; -.
KW Receptor.
FT NON_TER 1
FT NON_TER 48
FT NON_TER 48
SQ SEQUENCE 48 AA; 5811 MW; 5D5B18AAEE3AF4AF CRC64;

Query Match 1.8%; Score 10; DB 11; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHML 181
Db 8 LHCTRNVIHML 17

RESULT 12
Q9VHC8 ID Q9VHC8 PRELIMINARY; PRT; 167 AA.
AC Q9VHC8;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE GLUCAGON RECEPTOR (FRAGMENT).
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranolia; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PIUTARY;
RA Alexandre D., Anouar Y.;
RT "A cloned frog VIP/PACAP receptor exhibits pharmacological and tissue
RT distribution characteristics of both VPAC1 and VPAC2 receptors in
RT mammals.";
RL Endocrinology 0:0-0(1999).
DR EMBL: AF100642; AAD03600.1; -.
DR InterPro: IPR000832; -.
DR Pfam: PF00002; 7tm_2; 1.
DR PRINTS; PR00249; GPCRSECRETIN.
DR PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 167
FT NON_TER 167
SQ SEQUENCE 167 AA; 19505 MW; 07AF68131034F517 CRC64;

Query Match 1.8%; Score 10; DB 13; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
| | | | | | | | | |
Db 3 LVEGLYLHNL 12

Search completed: September 21, 2001, 17:13:34
Job time: 197 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 21, 2001, 17:08:12 ; Search time 14.41 Seconds
(without alignments)
773.031 Million cell updates

Title: US-09-236-468A-2
 Perfect score: 541
 Sequence: 1 MAWLGLSLHVGWGLMGSL.....DDILMEKPSRRPMESNPDTG 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0
Searched: 197339 seqs, 20590346 residues

Word size : 10
Total number of hits satisfying chosen parameters: 37

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 1000 summaries

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Database :
Issued_Patents_AA:*
1: /cgn2/6/ptodata/2/iaa/5A_COMB.pcp:*
2: /cgn2/6/ptodata/2/iaa/5B_COMB.pcp:*
3: /cgn2/6/ptodata/2/iaa/6A_COMB.pcp:*
4: /cgn2/6/ptodata/2/iaa/6B_COMB.pcp:*
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6: /cgn2/6/ptodata/2/iaa/backfiles1.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	541	100.0	541	3	US-08-468-0111A-2		Sequence 2, Appli
2	541	100.0	541	5	PCT-US95-07085-2		Sequence 2, Appli
3	60	11.1	60	3	US-08-468-0111A-9		Sequence 9, Appli
4	60	11.1	60	3	US-08-468-0111A-11		Sequence 11, Appli
5	60	11.1	60	3	US-08-468-0111A-15		Sequence 15, Appli
6	60	11.1	60	3	US-08-468-0111A-19		Sequence 19, Appli
7	59	10.9	59	3	US-08-468-0111A-23		Sequence 23, Appli
8	37	6.8	37	3	US-08-468-0111A-25		Sequence 25, Appli
9	37	6.8	50	3	US-08-468-0111A-30		Sequence 13, Appli
10	25	4.6	60	3	US-08-468-0111A-20		Sequence 20, Appli
11	25	4.6	515	2	US-08-468-249A-18		Sequence 18, Appli
12	25	4.6	585	1	US-08-468-249A-6		Sequence 6, Appli
13	25	4.6	585	2	US-08-142-439A-6		Sequence 125, App
14	25	4.6	585	2	US-08-142-551B-125		Sequence 6, Appli
15	25	4.6	585	2	US-08-869-477-6		Sequence 6, Appli
16	21	3.9	21	3	US-08-468-249A-19		Sequence 19, Appli
17	19	3.5	21	3	US-08-468-0111A-21		Sequence 21, Appli
18	19	3.5	449	1	US-08-142-439A-5		Sequence 5, Appli
19	18	3.3	449	2	US-08-869-477-5		Sequence 5, Appli
20	18	3.3	591	2	US-08-468-249A-20		Sequence 20, Appli
21	14	2.6	593	2	US-08-468-249A-21		Sequence 21, Appli
22	14	2.6	19	1	US-07-864-475A-7		Sequence 7, Appli
23	14	2.6	19	1	US-08-468-249A-7		Sequence 7, Appli
24	13	2.4	60	3	US-08-468-0111A-10		Sequence 10, Appli
25	13	2.4	458	1	US-08-1112-817C-2		Sequence 2, Appli
26	10	1.8	1324	2	US-08-811-897A-56		Sequence 56, Appli
27	10	1.8	162	1	US-08-468-0111A-17		Sequence 17, Appli
28	10	1.8	162	1	US-08-453-956-18		Sequence 18, Appli

28	10	1.8	162	1	US-08-086-631-18	Sequence 18, Appl
29	10	1.8	162	2	US-08-452-930-18	Sequence 18, Appl
30	10	1.8	162	5	PCT-US93-08174-18	Sequence 18, Appl
31	10	1.8	162	3	US-08-845-546-2	Sequence 10, Appl
32	10	1.8	222	3	US-08-845-546-10	Sequence 25, Appl
33	10	1.8	477	1	US-08-453-956-25	Sequence 25, Appl
34	10	1.8	477	1	US-08-096-631-25	Sequence 25, Appl
35	10	1.8	477	2	US-08-452-930-25	Sequence 25, Appl
36	10	1.8	477	5	PCT-US93-08174-25	Sequence 25, Appl
37	10	1.8	509	3	US-08-845-546-2	Sequence 2, Appl
38	10	1.8	553	3	US-08-845-546-12	Sequence 12, Appl

ALIGNMENTS

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RESULT      1
US-08-468-011A-2
; Sequence 2, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-2

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		Query Match	100.0%;	Score 541;	DB 3;	Length 541;
		Best Local Similarity	100.0%;	Pred. No. 0;		
		Matches 541;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAWLGASHVWGWMGLSCLLARAQLOSDGTTITTEEQIVLVLKAKVOCELNITAQLQEGE	60			
Db	1	MAWLGASHVWGWMGLSCLLARAQLOSDGTTITTEEQIVLVLKAKVOCELNITAQLQEGE	60			
QY	61	GNCPPEWDGLICPRGTVGKLSAVPCPPYIYDFNHKGVAFRHCNPNGTWDPMHSLUNKTWA	120			
Db	61	GNCPPEWDGLICPRGTVGKLSAVPCPPYIYDFNHKGVAFRHCNPNGTWDPMHSLUNKTWA	120			
QY	121	NYSCLAFRLPDIDISIGKOEFCERLYVMVTGYGSIFSFGSLAVAILTIIGYFRLHLCTRNVIH	180			

Db 121 NYSDCLRFQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHLCHCTRNYYH 180
QY 181 MHLFVFMRLRATSIYKDRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
Db 181 MHLFVFMRLRATSIYKDRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAAFAVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTVTHTSSQSOVAAAHAHWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTVTHTSSQSOVAAAHAHWCLSLAKLPR 480
QY 541 G 541
Db 541 G 541

RESULT 2

PCT-US95-07085-2
; Sequence 2, Application PC/TUS9507085
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07085
; FILING DATE: 05-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-393
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 541 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

PCT-US95-07085-2
Query Match 100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAWLGLASLHVWGMLGSCLLARAQLDSGTTTIEEQIVLVLKAKVQCELNITAQLQEGE 60
Db 1 MAWLGLASLHVWGMLGSCLLARAQLDSGTTTIEEQIVLVLKAKVQCELNITAQLQEGE 60
QY 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
Db 61 GNCFFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCNPNGTWDFMHSLNKTWA 120
QY 121 NYSDCLRFQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHLCHCTRNYYH 180
Db 121 NYSDCLRFQPDISIGKQECERLYVMYTVGYSISFGSLAVAILIIGYFRRHLCHCTRNYYH 180
QY 181 MHLFVFMRLRATSIYKDRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
Db 181 MHLFVFMRLRATSIYKDRVVAHIGVKELESIMODDPQNSIEATSVDKSOYIGCKIAV 240
QY 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAAFAVAWAVARAT 300
Db 241 VMFIYFLATNYWILVEGLYHNLIFVAFPSDTKYLWGFILIGWGFPAAFAVAWAVARAT 300
QY 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
Db 301 LADARCWELSGADIKWIYQAPILAAIGLNFILFLNTVRVLATKIWETNAVGHDTKQYRK 360
QY 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420
Db 361 LAKSTLVLVLFVGVHYIVFVCLPHSFTGLGWEIRHMCLEFFNSFGFFVSIYCYCNGEV 420
QY 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTVTHTSSQSOVAAAHAHWCLSLAKLPR 480
Db 421 QAEVKKMSRWNLSDVKMRTPPCGSRRCGSVLTVTHTSSQSOVAAAHAHWCLSLAKLPR 480
QY 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDE 540
Db 481 SPADSLTATSLYLAWSGVTSRTASHTLSTRSNKEDSGRQDDILMEKPSRPMESNPDE 540
QY 541 G 541
Db 541 G 541

RESULT 3

US-08-468-011A-9
; Sequence 9, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468.011A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 60 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-468-011A-9

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 214 IMQDDPQNSIEATSDVKSYIGCKIAVVMFYFLATNYWILVEGLYLNLIFFVAFFSDT 273
Db 1 IMQDDPQNSIEATSDVKSYIGCKIAVVMFYFLATNYWILVEGLYLNLIFFVAFFSDT 60

RESULT 4
US-08-468-011A-11
; Sequence 11, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTGDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-11

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 274 KYLWGFILIGWGFPAAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFIILF 333
Db 1 KYLWGFILIGWGFPAAFVAWAVARATLADARCWELSGADIKWIYQAPILAAIGLNFIILF 60

RESULT 5
US-08-468-011A-15
; Sequence 15, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTGDG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-15

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCHNPGCTWDFMHSLNKWTW 119
Db 1 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHKGVAFRHCHNPGCTWDFMHSLNKWTW 60

RESULT 6
US-08-468-011A-19
; Sequence 19, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven

;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
;; TITLE OF INVENTION: HLTDG74
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
;; ADDRESSEE: Stewart & Olstein
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07068-1739
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 INCH DISKETTE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: WORD PERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,011A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 60 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-468-011A-19

Query Match 11.1%; Score 60; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.6e-49;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 137 KQFECRLVMTVGVSGISFGLAVAILIYGFRRLLHCTRNVIHMLFVSFMLRATSIPIV 196
Db 1 KQFECRLVMTVGVSGISFGLAVAILIYGFRRLLHCTRNVIHMLFVSFMLRATSIPIV 60

RESULT 7
US-08-468-011A-23
;; Sequence 23, Application US/08468011A
;; Patent No. 6030804
;; GENERAL INFORMATION:
;; APPLICANT: Soppet, Daniel R
;; APPLICANT: Yi, Li
;; APPLICANT: Rosen, Craig A
;; APPLICANT: Ruben, Steven
;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
;; TITLE OF INVENTION: HLTDG74
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
;; ADDRESSEE: Stewart & Olstein
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07068-1739
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 INCH DISKETTE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: WORD PERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,011A
;; FILING DATE: 06-JUN-1995

;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 59 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-468-011A-23

Query Match 10.9%; Score 59; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.2e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 387 TGLGWEIRHMCLEFNFSGGFVSIYCYCNCEVOAEVKKMSRWNLSDMKRTPPCGS 445
Db 1 TGLGWEIRHMCLEFNFSGGFVSIYCYCNCEVOAEVKKMSRWNLSDMKRTPPCGS 59

RESULT 8
US-08-468-011A-25
;; Sequence 25, Application US/08468011A
;; Patent No. 6030804
;; GENERAL INFORMATION:
;; APPLICANT: Soppet, Daniel R
;; APPLICANT: Yi, Li
;; APPLICANT: Rosen, Craig A
;; APPLICANT: Ruben, Steven
;; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
;; TITLE OF INVENTION: HLTDG74
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
;; ADDRESSEE: Stewart & Olstein
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 07068-1739
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 INCH DISKETTE
;; COMPUTER: IBM PS/2
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: WORD PERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/468,011A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MULLINS, J.G.
;; REGISTRATION NUMBER: 33,073
;; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 37 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-468-011A-25

Query Match 6.8%; Score 37; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 8e-28;

;
; ADDRESS: Carella, Byrne, Bain, Gilfillan, Cecchi,
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: NJ

ZIP: 07068-1739
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,011A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.

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; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 20:

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; ; SEQUENCE CHARACTERISTICS:
; ; LENGTH: 60 amino acids
; ; TYPE: amino acid
; ; TOPOLOGY: linear
; ; MOLECULE TYPE: protein
US-08-468-011A-20

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Query Match	4.6%	Score 25	DB 3	Length 60
Best Local Similarity	100.0%	Pred. No.	2.5e-16	
Matches 25	Conservative 0	Mismatches 0	Indels	
QY	167	GYFRRLLHCTERNYIHMHLEVSFMLRA	191	
Db	31	GYFRRLLHCTERNYIHMHLEVSFMLRA	55	

US-08-468-249A-18
; Sequence 18, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME

ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street

```

:
: COUNTRY: USA
: ZIP: 02110-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
:

```

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: iPC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468.249A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,475
FILING DATE: 06-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/681,702
FILING DATE: 04-MAY-1991

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; ORGANISM: Didelphis virginiana
; US-08-142-439A-6

Query Match      4.6%; Score 25; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 167 GYFRRLLHCTRNYIHMHFLVFSFMLRA 191
      |||||
DB 207 GYFRRLLHCTRNYIHMHFLVFSFMLRA 231

RESULT 13
US-08-142-551B-125
; Sequence 125, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142.551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..585
; OTHER INFORMATION: /note= "PTH receptor"
US-08-142-551B-125

Query Match      4.6%; Score 25; DB 2; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 25; Conservative 0; Mismatches 0; Indels

QY 167 GYFRRLLHCTRNYIHMHFLVFSFMLRA 191
      |||||
DB 207 GYFRRLLHCTRNYIHMHFLVFSFMLRA 231

RESULT 12
US-08-142-439A-6
; Sequence 6, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360 No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

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;
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-011A-21

Query Match 3.9%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 197 KDRVVHAHIGVKESLIMQD 217
Db 1 KDRVVHAHIGVKESLIMQD 21

RESULT 17
US-08-142-439A-5
; Sequence 5, Application US/08142439A
; Patent No. 5670360
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5670360o No. 5670360disk of No. 5670360th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439A
; FILING DATE: 24-NOV-93
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION NUMBER: PCT/EP93/00697
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-869-477-5

;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-142-439A-5

Query Match 3.5%; Score 19; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 FRRLHCTRNYYHMLFVSF 187
Db 167 FRRLHCTRNYYHMLFVSF 185

RESULT 18
US-08-869-477-5
; Sequence 5, Application US/08869477
; Patent No. 5846747
; GENERAL INFORMATION:
; APPLICANT: Thorens, Bernard
; TITLE OF INVENTION: Receptor for the Glucagon-Like-Peptide-1
; TITLE OF INVENTION: (GLP-1)
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5846747o No. 5846747disk of No. 5846747th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/869,477
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,439
; FILING DATE: 24-NOV-93
; APPLICATION NUMBER: DK 398/92
; FILING DATE: 25-MAR-92
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/00697
; FILING DATE: 23-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: 38,711
; REFERENCE/DOCKET NUMBER: 3756.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Rattus norvegicus
; STRAIN: Sprague-Dawley
; US-08-869-477-5
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```
Query Match      3.5%; Score 19; DB 2; Length 449;
Best Local Similarity 100.0%; Pred. No. 6.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 169 FRLHCTRYIHMLFVSF 187
      |||||
Db 167 FRLHCTRYIHMLFVSF 185

RESULT 19
US-08-468-249A-20
; Sequence 20, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 591 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-249A-21

Query Match      3.3%; Score 18; DB 2; Length 593;
Best Local Similarity 100.0%; Pred. No. 7.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262
      |||||
Db 290 YFLATNYWILVEGLYH 307

RESULT 21
US-07-864-475A-7
; Sequence 7, Application US/07864475A
; Patent No. 5494806
; GENERAL INFORMATION:
; APPLICANT: Segre, Gino V.
; APPLICANT: Kronenberg, Henry M.
; APPLICANT: Abou-Samra, Abdul-Badi
; APPLICANT: Juppner, Harald
; APPLICANT: Potts, John T. [Jr.]
; APPLICANT: Schipani, Ernestina
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

Query Match      3.3%; Score 18; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 7.6e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 245 YFLATNYWILVEGLYH 262
      |||||
Db 290 YFLATNYWILVEGLYH 307

RESULT 20
US-08-468-249A-21
; Sequence 21, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
```

```

, COMPUTER: IBM PS/2 Model 502 or 55SX
, OPERATING SYSTEM: MS-DOS (Version 5.0)
, SOFTWARE: WordPerfect (Version 5.1)
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/07/864,475A
, FILING DATE: 04-06-1992
, CLASSIFICATION: 435
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 07/681,702
, FILING DATE: 05-04-1991
, ATTORNEY/AGENT INFORMATION:
, NAME: Paul T. Clark
, REGISTRATION NUMBER: 30,162
, REFERENCE/DOCKET NUMBER: 00786/071002
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (617) 542-5070
, TELEFAX: (617) 542-8906
, TELEX: 200154
, INFORMATION FOR SEQ ID NO: 7:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 19
, TYPE: amino acid
, STRANDEDNESS:
, TOPOLOGY: linear
US-07-864-475A-7

```

Query Match 2.6%; Score 14; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels

RESULT 22
US-08-468-249A-7
; Sequence 7, Application US/08468249A
; Patent No. 5886148
; GENERAL INFORMATION:
; APPLICANT: Segre et al., Gino V.
; TITLE OF INVENTION: PARATHYROID HORMONE RECEPTOR AND DNA
; TITLE OF INVENTION: ENCODING SAME
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,249A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/864,475
; FILING DATE: 06-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,702
; FILING DATE: 04-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/071003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070

```

; TELEFAX: 617/542-8906
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-249A-7

```

Query Match 2.6%; Score 14; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels

```

RESULT 23
US-08-468-011A-10
; Sequence 10, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA: US/08/468-011A
; APPLICATION NUMBER: US/08/468-011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 60 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-011A-10

```

Query Match	2.6%	Score 14;	DB 3;	Length 60;
Best Local Similarity	100.0%;	Pred. NO. 5.9e-06;		
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	249	TNYYWILVEGLYLH	262	
Db	36	TNYYWILVEGLYLH	49	

RESULT 24
US-08-112-817C-2
; Sequence 2, Application US/08112817C
; Patent No. 5573928
; GENERAL INFORMATION:
; APPLICANT: Hsiung, Hansen M.
; APPLICANT: Smith, Dennis P.
; APPLICANT: Zhang, Xing-Yue
; TITLE OF INVENTION: PORCINE VASOACTIVE INTESTINAL PEPTIDE
; TITLE OF INVENTION: RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh IIfx compatible
; OPERATING SYSTEM: System 7
; SOFTWARE: Microsoft Word for Macintosh v.5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/112.817C
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy, Richard B.
; REGISTRATION NUMBER: 35,296
; REFERENCE/DOCKET NUMBER: X-9293
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3589
; TELEFAX: 317-276-1294
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-112-817C-2

Query Match 2.4%; Score 13; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIHMLF 184
| | | | | | | | | |
Db 171 LHCTRNVIHMLF 183

RESULT 25
US-08-811-897A-56
; Sequence 56, Application US/08811897A
; Patent No. 5858787
; GENERAL INFORMATION:
; APPLICANT: ONDA, Haruo
; APPLICANT: OHTAKI, Tetsuya
; APPLICANT: MASUDA, Yasushi
; APPLICANT: KITADA, Chieko
; APPLICANT: ISHIBASHI, Yoshihiro
; APPLICANT: HOSoya, Masaki
; APPLICANT: OGI, Kazuhiro
; APPLICANT: MIYAMOTO, Yasunori
; APPLICANT: HABA, Yugo
; APPLICANT: SHIMAMOTO, No. 58587871c
; TITLE OF INVENTION: PACAP RECEPTOR PROTEIN, METHOD FOR PREPARING
; TITLE OF INVENTION: SAID PROTEIN, AND USE THEREOF
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &

; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811.897A
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/202,986
; FILING DATE: February 25, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: RESNICK, David S.
; REGISTRATION NUMBER: 34235
; REFERENCE/DOCKET NUMBER: 44168-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1324 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-811-897A-56

Query Match 2.4%; Score 13; DB 2; Length 1324;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 172 LHCTRNVIHMLF 184
| | | | | | | | | |
Db 173 LHCTRNVIHMLF 185

RESULT 26
US-08-468-011A-17
; Sequence 17, Application US/08468011A
; Patent No. 6030804
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R
; APPLICANT: Yi, Li
; APPLICANT: Rosen, Craig A
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: G-Protein Parathyroid Hormone receptor
; TITLE OF INVENTION: HLTG74
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
; ADDRESSEE: Stewart & Oistein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: NJ
; COUNTRY: USA
; ZIP: 07068-1739
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468.011A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-458 (PF201)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-011A-17

Query Match 1.8%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ANYSDCLRFL 129
Db 1 ANYSDCLRFL 10
|||||

RESULT 27
US-08-453-956-18
; Sequence 18, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,956
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-956-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
Db 99 LVEGLYLHNL 108
|||||

RESULT 28
US-08-086-631-18
; Sequence 18, Application US/08086631
; Patent No. 5776725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/086,631
; FILING DATE: July 1, 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-086-631-18

Query Match 1.8%; Score 10; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
Db 99 LVEGLYLHNL 108
|||||

RESULT 29
US-08-452-930-18
; Sequence 18, Application US/08452930
; Patent No. 5919635
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/452,930
;; FILING DATE: 30-MAY-1995
;; CLASSIFICATION: .435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/086,631
;; FILING DATE: July 1, 1993
;; APPLICATION NUMBER: US 07/938,331
;; FILING DATE: 28-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 990008.424C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-622-4900
;; TELEFAX: 206-682-6031
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US93-08174-18

Query Match 1.8%; Score 10; DB 2; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYHLNL 264
| | | | | | | | | |
Db 99 LVEGLYHLNL 108

RESULT 30
PCT-US93-08174-18
; Sequence 18, Application PC/TUS9308174
; GENERAL INFORMATION:
; APPLICANT: NAME: ZymoGenetics, Inc.
; APPLICANT: STREET: 4225 Roosevelt Way North East
; APPLICANT: CITY: Seattle, Washington
; APPLICANT: COUNTRY: United States
; APPLICANT: POSTAL CODE: 98105
; APPLICANT: TELEPHONE: (206) 547-80808
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/08174
; FILING DATE: 30-AUG-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:

;; NAME: McMasters, David D.
;; REGISTRATION NUMBER: 33,963
;; REFERENCE/DOCKET NUMBER: 990008.424C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-622-4900
;; TELEFAX: 206-682-6031
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; PCT-US93-08174-18

Query Match 1.8%; Score 10; DB 5; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 255 LVEGLYHLNL 264
| | | | | | | | | |
Db 99 LVEGLYHLNL 108

RESULT 31
US-08-845-546-10
; Sequence 10, Application US/08845546
; Patent No. 6077949
; GENERAL INFORMATION:
; APPLICANT: Munroe, Donald
; APPLICANT: Gupta, Ashwani
; APPLICANT: Vyas, Tejpal
; APPLICANT: McCallum, Kirk
; APPLICANT: Fan, Ermei
; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,546
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8607-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-845-546-10

Query Match 1.8%; Score 10; DB 3; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.11;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNHYM 181
 |||||
Db 20 LHCTRNHYM 29

RESULT 32

US-08-453-956-25
; Sequence 25, Application US/08453956
; Patent No. 5770445
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/453,956
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-956-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
 |||||
Db 243 LVEGLYLHNL 252

RESULT 33

US-08-086-631-25
; Sequence 25, Application US/08086631
; Patent No. 5776725
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE

STATE: WA
COUNTRY: USA
ZIP: 99104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/086,631
FILING DATE: July 1, 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,331
FILING DATE: 28-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 990008.424C1
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-086-631-25

Query Match 1.8%; Score 10; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
 |||||
Db 243 LVEGLYLHNL 252

RESULT 34

US-08-452-930-25
; Sequence 25, Application US/08452930
; Patent No. 5919635
; GENERAL INFORMATION:
; APPLICANT: Kindsvogel, Wayne R.
; TITLE OF INVENTION: GLUCAGON RECEPTORS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY
; STREET: 6300 COLUMBIA CENTER
; CITY: SEATTLE
; STATE: WA
; COUNTRY: USA
; ZIP: 99104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,930
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,631
; FILING DATE: July 1, 1993
; APPLICATION NUMBER: US 07/938,331
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 990008.424C1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-452-930-25

Query Match 1.8%; Score 10; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 255 LVEGLYLHNL 264
|||||

DB 243 LVEGLYLHNL 252

RESULT 35

PCT-US93-08174-25

Sequence 25, Application PC/TUS9308174

GENERAL INFORMATION:

APPLICANT:

APPLICANT: NAME: ZymoGenetics, Inc.

APPLICANT: STREET: 4225 Roosevelt Way North East

APPLICANT: CITY: Seattle, Washington

APPLICANT: COUNTRY: United States

APPLICANT: POSTAL CODE: 98105

APPLICANT: TELEPHONE: (206) 547-8080

TITLE OF INVENTION: GLUCAGON RECEPTORS

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED AND BERRY

STREET: 6300 COLUMBIA CENTER

CITY: SEATTLE

STATE: WA

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/08174

FILING DATE: 30-AUG-1993

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/086,631

FILING DATE: July 1, 1993

APPLICATION NUMBER: US 07/938,331

FILING DATE: 28-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: McMasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 990008.424C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

TELEFAX: 206-682-6031

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 477 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US93-08174-25

Query Match 1.8%; Score 10; DB 5; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.22;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 255 LVEGLYLHNL 264
|||||

DB 243 LVEGLYLHNL 252

RESULT 36

US-08-845-546-2

Sequence 2, Application US/08845546

Patent No. 6077949

GENERAL INFORMATION:

APPLICANT: Munroe, Donald

APPLICANT: Gupta, Ashwani

APPLICANT: Vyas, Tejal

APPLICANT: McCallum, Kirk

APPLICANT: Fan, Ermei

TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,546

FILING DATE: 24-APR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Friebe, Thomas E.

REGISTRATION NUMBER: 29,258

REFERENCE/DOCKET NUMBER: 8607-018

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 509 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-845-546-2

Query Match 1.8%; Score 10; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LHCTRNVIHM 181
|||||

DB 165 LHCTRNVIHM 174

RESULT 37

US-08-845-546-12

Sequence 12, Application US/08845546

Patent No. 6077949

GENERAL INFORMATION:

APPLICANT: Munroe, Donald

APPLICANT: Gupta, Ashwani

APPLICANT: Vyas, Tejal

APPLICANT: McCallum, Kirk

APPLICANT: Fan, Ermei

```

; TITLE OF INVENTION: CLONED GLUCAGON-LIKE PEPTIDE
; TITLE OF INVENTION: 2 RECEPTORS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,546
; FILING DATE: 24-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Friebe, Thomas E.
; REGISTRATION NUMBER: 29,258
; REFERENCE/DOCKET NUMBER: 8607-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-845-546-12

```

```

Query Match 1.8%; Score 10; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 172 LHCTRNHYHM 181
Db 206 LHCTRNHYHM 215

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Search completed: September 21, 2001, 17:10:15
Job time: 123 sec

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